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(54) **GENE EXPRESSION MARKERS FOR COLORECTAL CANCER PROGNOSIS**

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(51) **Int. Cl.**
C12Q 1/68 (2006.01)

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(58) **Field of Classification Search** .... None
See application file for complete search history.

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(57) **ABSTRACT**

A method of predicting clinical outcome in a subject diagnosed with colorectal cancer comprising determining evidence of the expression of one or more predictive RNA transcripts or their expression products in a biological sample of cancer cells obtained from the subject.

18 Claims, 1 Drawing Sheet

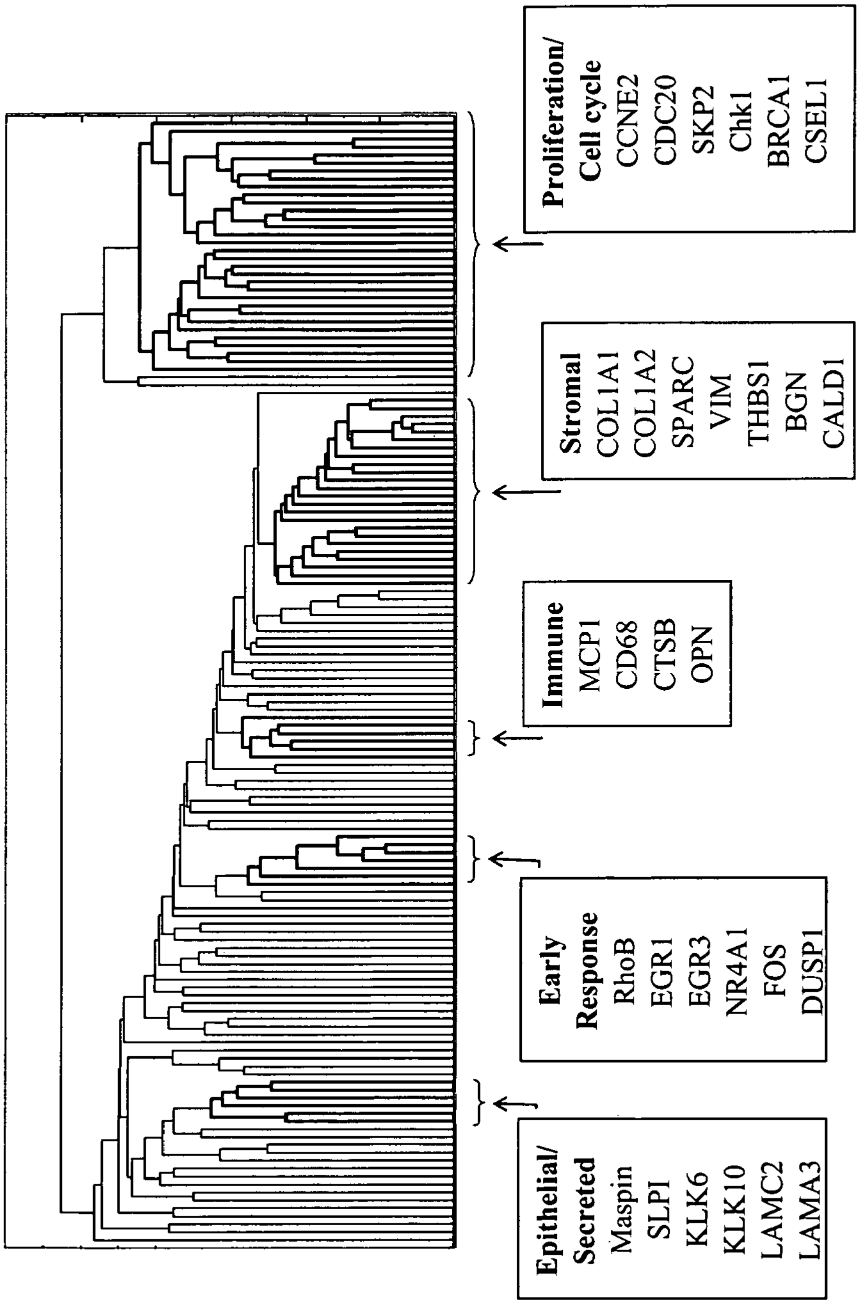
Epithelial/ Secreted
Maspin
SLPI
KLK6
KLK10
LAMC2
LAMA3
Early Response
RhoB
EGR1
EGR3
NR4A1
FOS
DUSP1
Immune
MCP1
CD68
CTSB
OPN
Stromal
COL1A1
COL1A2
SPARC
VIM
THBS1
BGN
CALD1
Proliferation/ Cell cycle
CCNE2
CDC20
SKP2
Chk1
BRCA1
CSEL1

FIGURE 1

GENE EXPRESSION MARKERS FOR COLORECTAL CANCER PROGNOSIS

CROSS-REFERENCE TO RELATED APPLICATIONS

This is a non-provisional application filed under 37 C.F.R. 1.53(b) claiming priority under 35 U.S.C. §119(e) to provisional Application Ser. No. 60/758,392 filed Jan. 11, 2006 and to provisional Application Ser. No. 60/800,277 filed May 12, 2006 and to provisional Application Ser. No. 60/810,077 filed May 31, 2006 all of which are incorporated herein by reference in their entirety.

BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention provides genes and gene sets, the expression levels of which are useful for predicting outcome of colorectal cancer.

2. Description of Related Art

Colorectal cancer is the number two cause of cancer-related death in the United States and the European Union, accounting for 10% of all cancer-related deaths. Although colon cancer and rectal cancer may represent identical or similar disease at the molecular level, surgery for rectal cancer is complicated by anatomical issues. Possibly for this reason, the rate of local recurrence for rectal cancer is significantly higher than for colon cancer, and so the treatment approach is significantly different. Approximately 100,000 colon cancers are newly diagnosed each year in the United States, with about 65% of these being diagnosed as stage II/III colorectal cancer as discussed below.

Refining a diagnosis of colorectal cancer involves evaluating the progression status of the cancer using standard classification criteria. Two classification systems have been widely used in colorectal cancer, the modified Duke's or Astler-Coller staging system (Stages A-D) (Astler V B, Coller F A., *Ann Surg* 1954; 139:846-52), and more recently TNM staging (Stages I-IV) as developed by the American Joint Committee on Cancer (*AJCC Cancer Staging Manual,* 6th Edition, Springer-Verlag, New York, 2002). Both systems apply measures of the spread of the primary tumor through layers of colon or rectal wall to the adjacent organs, lymph nodes and distant sites to evaluate tumor progression. Estimates of recurrence risk and treatment decisions in colon cancer are currently based primarily on tumor stage.

There are approximately 33,000 newly diagnosed Stage II colorectal cancers each year in the United States. Nearly all of these patients are treated by surgical resection of the tumor and, in addition, about 40% are currently treated with chemotherapy based on 5-fluorouracil (5-FU). The decision whether to administer adjuvant chemotherapy is not straightforward. The five-year survival rate for Stage II colon cancer patients treated with surgery alone is approximately 80%. Standard adjuvant treatment with 5-FU+leucovorin (folinic acid) demonstrates an absolute benefit of only 2-4% in this population and shows significant toxicity, including a rate of toxic death from chemotherapy as high as 1%. Thus, a large number of patients receive toxic therapy from which only a few benefit.

A test capable of prognosis after surgery in Stage II colorectal cancer patients would be of great benefit for guiding treatment decisions for these patients.

The benefit of chemotherapy in Stage III colon cancer is more evident than it is in Stage II. A large proportion of the 31,000 patients annually diagnosed with Stage III colon cancer receive 5-FU-based adjuvant chemotherapy, and the absolute benefit of 5-FU+leucovorin in this setting is around 18-24%, depending on the particular regimen employed. Current standard-of-care chemotherapy treatment for Stage III colon cancer patients (5-FU+leucovorin or 5-FU+leucovorin+oxaliplatin) is moderately effective, achieving an improvement in 5-yr survival rate from about 50% (surgery alone) to about 65% (5-FU+leucovorin) or 70% (5-FU+leucovorin+oxaliplatin). Treatment with 5-FU+leucovorin alone or in combination with oxaliplatin is accompanied by a range of adverse side-effects, including toxic death in approximately 1% of patients treated. Furthermore, the three-year survival rate for Stage III colon cancer patients treated with surgery alone is about 47% and it has not been established whether a subset of Stage III patients exists for which recurrence risk resembles that observed for Stage II patients.

A test that would quantify recurrence risk based on molecular markers rather than tumor stage alone would be useful for identifying a subset of Stage III patients that may not require adjuvant therapy to achieve acceptable outcomes.

Staging of rectal tumors is carried out based on similar criteria as for colon tumor staging, although there are some differences resulting for example from differences in the arrangement of the draining lymph nodes. As a result, Stage II/III rectal tumors bear a reasonable correlation to Stage II/III colon tumors as to their state of progression. As noted above, the rate of local recurrence and other aspects of prognosis differ between rectal cancer and colon cancer, and these differences may arise from difficulties in accomplishing total resection of rectal tumors. Nevertheless, there is no compelling evidence that there is a difference between colon cancer and rectal cancer as to the molecular characteristics of the respective tumors. Prognostic tests for rectal cancer would have utility similar in nature as described for colon cancer prognostic tests and the same prognostic markers might well apply to both cancer types.

In addition, there is a clear need for safer and more efficacious drugs for the treatment of colon cancer. Current chemotherapy for colon cancer is based on the relatively crude approach of administering drugs that generally interfere with the proliferation of dividing cells. Recent clinical studies have demonstrated the feasibility of developing improved drugs based on detailed molecular understanding of particular cancer types and subtypes. For example, the HER2 (ERBB2) gene is amplified and the HER2 protein is overexpressed in a subset of breast cancers; HERCEPTIN® (Genentech, Inc.) a drug developed to target HER2, is indicated only for those patients who have an higher than normal copy number of HER2 as demonstrated by fluorescent in situ hybridization (FISH) or a high level of HER2 expression as demonstrated by immunohistochemistry. Genes, whose expression is associated with clinical outcome in human cancer patients, are a valuable resource for selection of targets for drug compound screening and further drug development activities.

Molecularly targeted drugs, such as HERCEPTIN® (Genentech, Inc.) can be developed and commercialized in conjunction with a diagnostic test that can identify patients who are likely to benefit from the drug; one aspect of such a test is the identification of those patients likely to have a positive outcome without any treatment other than surgery. For example, 80% of Stage II colon cancer patients survive five years or more when treated with surgery alone. Gene markers that identify patients more likely to be among the 20% whose cancer will recur without additional treatment are useful in drug development, for example in screening patients for inclusion in a clinical trial.

SUMMARY OF THE INVENTION

In one aspect, the present invention concerns a method for predicting the clinical outcome in a subject diagnosed with colorectal cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 1A-B, 2A-B, 3A-B, 4A-B, 5A-B, 6 and/or 7, or their expression products, in a biological sample comprising cancer cells obtained from said subject wherein: (a) evidence of increased expression of one or more of the genes listed in Table 1A, 2A, 3A, 4A, and/or 5A, or the corresponding expression product, indicates a decreased likelihood of a positive clinical outcome; and (b) evidence of increased expression of one or more of the genes listed in Table 1B, 2B, 3B, 4B and/or 5B, or the corresponding expression product, indicates an increased likelihood of a positive clinical outcome. It is contemplated that if the likelihood of positive clinical outcome is predicted to be decreased said patient is subjected to further therapy following said surgical removal. It is further contemplated that the therapy is chemotherapy and/or radiation therapy.

The clinical outcome of the method of the invention may be expressed, for example, in terms of Recurrence-Free Interval (RFI), Overall Survival (OS), Disease-Free Survival (DFS), or Distant Recurrence-Free Interval (DRFI).

In one embodiment, the cancer is Dukes B (stage II) or Dukes C (stage III) colorectal cancer.

In another aspect, the invention concerns a method of predicting the duration of Recurrence-Free Interval (RFI) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colorectal cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 1A, 5A, 1B, and/or 5B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes listed in Table 1A or 5A, or the corresponding expression product, indicates that said RFI is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 1B, or 5B, or the corresponding expression product, indicates that said RFI is predicted to be longer.

In another aspect, the invention concerns a method of predicting Overall Survival (OS) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 2A and/or 2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes listed in Table 2A, or the corresponding expression product, indicates that said OS is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 2B, or the corresponding expression product, indicates that said OS is predicted to be longer.

In another aspect, the invention concerns a method of predicting Disease-Free Survival (DFS) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 3A, and/or 3B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes listed in Table 3A, or the corresponding expression product, indicates that said DFS is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 3B, or the corresponding expression product, indicates that said DFS is predicted to be longer.

In another aspect, the invention concerns a method of predicting the duration of Distant Recurrence-Free Interval (DRFI) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 4A and/or 4B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes listed in Table 4A, or the corresponding expression product, indicates that said DRFI is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 4B, or the corresponding expression product, indicates that said DRFI is predicted to be longer.

In another aspect, the invention concerns a method of predicting clinical outcome for a subject diagnosed with colorectal cancer following surgical resection of said cancer, comprising determining evidence of the expression level of one or more predictive RNA transcripts listed in Tables 1.2A-B, 2.2A-B, 3.2A-B, 4.2A-B, 5.2A-B, 6.2 and/or 7.2, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 1.2A, 2.2A, 3.2A, 4.2A and/or 5.2A, or the corresponding expression product, indicates a decreased likelihood of a positive clinical outcome; and (b) evidence of increased expression of one or more of the genes listed in Table 1.2B, 2.2B, 3.2B, 4.2B and/or 5.2B, or the corresponding expression product, indicates an increased likelihood of a positive clinical outcome.

In another aspect, the invention concerns a method of predicting the duration of Recurrence-Free Interval (RFI) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colorectal cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 1.2A, 1.2B, 5.2A and/or 5.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 1.2A or 5.2A, or the corresponding expression product, indicates that said RFI is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 1.2B or 5.2B, or the corresponding expression product, indicates that said RFI is predicted to be longer.

In another aspect, the invention concerns a method of predicting Overall Survival (OS) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 2.2A and/or 2.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 2.2A, or the corresponding expression product, indicates that said OS is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 2.2B, or the corresponding expression product, indicates that said OS is predicted to be longer.

In another aspect, the invention concerns a method of predicting Disease-Free Survival (DFS) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 3.2A and/or 3.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 3.2A, or the corresponding expression product, indicates that said DFS is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 3.2B, or the corresponding expression product, indicates that said DFS is predicted to be longer.

In another aspect, the invention concerns a method of predicting the duration of Distant Recurrence-Free Interval (DRFI) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 4.2A and/or 4.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 4.2A, or the corresponding expression product, indicates that said DRFI is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 4.2B, or the corresponding expression product, indicates that said DRFI is predicted to be longer.

In another aspect, the invention concerns a method of predicting clinical outcome for a subject diagnosed with colorectal cancer following surgical resection of said cancer, comprising determining evidence of the expression level of one or more predictive RNA transcripts listed in Tables 1A-B, 1.2A-B, 2A-B, 2.2A-B, 3A-B, 3.2A-B, 4A-B, 4.2A-B, 5A-B, 5.2A-B, 6, 6.2, 7 and/or 7.2, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 1A, 1.2A, 2A, 2.2A, 3A, 3.2A, 4A, 4.2A, 5A and/or 5.2A, or the corresponding expression product, indicates a decreased likelihood of a positive clinical outcome; and (b) evidence of increased expression of one or more of the genes listed in Table 1B, 1.2B, 2B, 2.2B, 3B, 3.2B, 4B, 4.2B, 5B and/or 5.2B, or the corresponding expression product, indicates an increased likelihood of a positive clinical outcome.

In another aspect, the invention concerns a method of predicting the duration of Recurrence-Free Interval (RFI) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colorectal cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 1A, 1.2A, 1B, 1.2B, 5A, 5.2A, 5B and/or 5.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 1A, 1.2A, 5A and/or 5.2A, or the corresponding expression product, indicates that said RFI is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 1B, 1.2B, 5B and/or 5.2B, or the corresponding expression product, indicates that said RFI is predicted to be longer.

In another aspect, the invention concerns a method of predicting Overall Survival (OS) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 2A, 2.2A, 2B and/or 2.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 2A and/or 2.2A, or the corresponding expression product, indicates that said OS is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 2B and/or 2.2B, or the corresponding expression product, indicates that said OS is predicted to be longer.

In another aspect, the invention concerns a method of predicting Disease-Free Survival (DFS) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 3A, 3.2A, 3B and/or 3.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 3A and/or 3.2A, or the corresponding expression product, indicates that said DFS is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 3B and/or 3.2B, or the corresponding expression product, indicates that said DFS is predicted to be longer.

In another aspect, the invention concerns a method of predicting the duration of Distant Recurrence-Free Interval (DRFI) in a subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colon cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts listed in Tables 4A, 4.2A, 4B and/or 4.2B, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 4A and/or 4.2A, or the corresponding expression product, indicates that said DRFI is predicted to be shorter; and (b) evidence of increased expression of one or more of the genes listed in Table 4B and/or 4.2B, or the corresponding expression product, indicates that said DRFI is predicted to be longer.

In another aspect, the invention concerns a method of predicting clinical outcome in a subject diagnosed with Dukes B (stage II) colorectal cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts selected from the group consisting of ALCAM, CD24, CDH11, CENPE, CLTC, CYR61, EMR3, ICAM2, LOX, MADH2, MGAT5, MT3, NUFIP1, PRDX6, SIR2, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, WIF, CAPG, CD28, CDC20, CKS1B, DKK1, HSD17B2, and MMP7, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes selected from the group consisting of ALCAM, CD24, CDH11, CENPE, CLTC, CYR61, EMR3, ICAM2, LOX, MADH2, MGAT5, MT3, NUFIP1, PRDX6, SIR2, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, and WIF, or the corresponding expression product, indicates a decreased likelihood of positive clinical outcome; and (b) evidence of increased expression of one or more of the genes selected from the group consisting of CAPG, CD28, CDC20, CKS1B, DKK1, HSD17B2, and MMP7, or the corresponding expression product, indicates an increased likelihood of positive clinical outcome.

In another aspect, the invention concerns a method of predicting clinical outcome in a subject diagnosed with Dukes C (stage III) colorectal cancer following surgical resection of said cancer, comprising determining the expression level of one or more predictive RNA transcripts selected from the group consisting of CAPG, CD28, CKS1B, CYR61, DKK1, HSD17B2, LOX, MMP7, SIR2, ALCAM, CD24, CDC20, CDH11, CENPE, CLTC, EMR3, ICAM2, MADH2,

MGAT5, MT3, NUFIP1, PRDX6, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, and WIF, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes selected from the group consisting of CAPG, CD28, CKS1B, CYR61, DKK1, HSD17B2, LOX, MMP7, and SIR2, or the corresponding expression product, indicates a decreased likelihood of positive clinical outcome; and (b) evidence of increased expression of one or more of the genes selected from the group consisting of ALCAM, CD24, CDC20, CDH11, CENPE, CLTC, EMR3, ICAM2, MADH2, MGAT5, MT3, NUFIP1, PRDX6, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, and WIF, or the corresponding expression product, indicates an increased likelihood of positive clinical outcome.

For all aspects of the method of the invention, determining the expression level of one or more genes may be obtained, for example, by a method of gene expression profiling. The method of gene expression profiling may be, for example, a PCR-based method.

For all aspects of the invention, the expression levels of the genes may be normalized relative to the expression levels of one or more reference genes, or their expression products.

For all aspects of the invention, the subject preferably is a human patient.

For all aspects of the invention, the method may further comprise determining evidence of the expression levels of at least two of said genes, or their expression products. It is further contemplated that the method of the invention may further comprise determining evidence of the expression levels of at least three of said genes, or their expression products. It is also contemplated that the method of the invention may further comprise determining evidence of the expression levels of at least four of said genes, or their expression products. It is also contemplated that the method of the invention may further comprise determining evidence of the expression levels of at least five of said genes, or their expression products.

For all aspects of the invention, the method may further comprise the step of creating a report summarizing said prediction.

For all aspects of the invention, it is contemplated that for every increment of an increase in the level of one or more predictive RNA transcripts or their expression products, the patient is identified to show an incremental increase in clinical outcome.

For all aspects of the invention, the determination of expression levels may occur more than one time. For all aspects of the invention, the determination of expression levels may occur before the patient is subjected to any therapy following surgical resection.

In a different aspect the invention is directed to a report comprising the predicted clinical outcome in a subject diagnosed with colorectal cancer following surgical resection of said cancer, comprising a prediction of clinical outcome based on information comprising the expression level of one or more predictive RNA transcripts listed in Tables 1A-B, 2A-B, 3A-B, 4A-B, 5A-B, 6 and/or 7, or their expression products, in a biological sample comprising cancer cells obtained from said subject wherein: (a) evidence of increased expression of one or more of the genes listed in Table 1A, 2A, 3A, 4A, and/or 5A, or the corresponding expression product, indicates a decreased likelihood of a positive clinical outcome; and (b) evidence of increased expression of one or more of the genes listed in Table 1B, 2B, 3B, 4B and/or 5B, or the corresponding expression product, indicates an increased likelihood of a positive clinical outcome. The clinical outcome of the report of the invention may be expressed, for example, in terms of Recurrence-Free Interval (RFI), Overall Survival (OS), Disease-Free Survival (DFS), or Distant Recurrence-Free Interval (DRFI). In one embodiment that cancer is Dukes B (stage II) or Dukes C (stage III) colorectal cancer. The prediction of clinical outcome may comprise an estimate of the likelihood of a particular clinical outcome for a subject or may comprise the classification of a subject into a risk group based on said estimate.

In another aspect the invention is directed to a report predicting clinical outcome for a subject diagnosed with colorectal cancer following surgical resection of said cancer, comprising a prediction of clinical outcome based on information comprising the expression level of one or more predictive RNA transcripts listed in Tables 1.2A-B, 2.2A-B, 3.2A-B, 4.2A-B, 5.2A-B, 6.2 and/or 7.2, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 1.2A, 2.2A, 3.2A, 4.2A and/or 5.2A, or the corresponding expression product, indicates a decreased likelihood of a positive clinical outcome; and (b) evidence of increased expression of one or more of the genes listed in Table 1.2B, 2.2B, 3.2B, 4.2B and/or 5.2B, or the corresponding expression product, indicates an increased likelihood of a positive clinical outcome. The clinical outcome of the report of the invention may be expressed, for example, in terms of Recurrence-Free Interval (RFI), Overall Survival (OS), Disease-Free Survival (DFS), or Distant Recurrence-Free Interval (DRFI). In one embodiment that cancer is Dukes B (stage II) or Dukes C (stage III) colorectal cancer. The prediction of clinical outcome may comprise an estimate of the likelihood of a particular clinical outcome for a subject or may comprise the classification of a subject into a risk group based on said estimate.

In another aspect, the invention concerns a report predicting clinical outcome for a subject diagnosed with colorectal cancer following surgical resection of said cancer, comprising a prediction of clinical outcome based on information comprising the expression level of one or more predictive RNA transcripts listed in Tables A-B, 1.2A-B, 2A-B, 2.2A-B, 3A-B, 3.2A-B, 4A-B, 4.2A-B, 5A-B, 5.2A-B, 6, 6.2, 7 and/or 7.2, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein (a) evidence of increased expression of one or more of the genes listed in Table 1A, 1.2A, 2A, 2.2A, 3A, 3.2A, 4A, 4.2A, 5A and/or 5.2A, or the corresponding expression product, indicates a decreased likelihood of a positive clinical outcome; and (b) evidence of increased expression of one or more of the genes listed in Table 1B, 1.2B, 2B, 2.2B, 3B, 3.2B, 4B, 4.2B, 5B and/or 5.2B, or the corresponding expression product, indicates an increased likelihood of a positive clinical outcome. The prediction of clinical outcome may comprise an estimate of the likelihood of a particular clinical outcome for a subject or may comprise the classification of a subject into a risk group based on said estimate.

In another aspect the invention is directed to a report predicting clinical outcome in a subject diagnosed with Dukes B (stage II) colorectal cancer following surgical resection of said cancer, comprising a prediction of clinical outcome based on information comprising the expression level of one or more predictive RNA transcripts selected from the group consisting of ALCAM, CD24, CDH11, CENPE, CLTC, CYR61, EMR3, ICAM2, LOX, MADH2, MGAT5, MT3, NUFIP1, PRDX6, SIR2, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, WIF, CAPG, CD28, CDC20, CKS1B, DKK1, HSD17B2, and MMP7, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes selected from the group consisting of ALCAM, CD24, CDH11, CENPE, CLTC, CYR61, EMR3, ICAM2, LOX, MADH2, MGAT5, MT3, NUFIP1, PRDX6, SIR2, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, and WIF, or the corresponding expression product, indicates a decreased likelihood of positive clinical outcome; and (b) evidence of increased expression of one or more of the genes selected from the group consisting of CAPG, CD28, CDC20, CKS1B, DKK1, HSD17B2, and MMP7, or the corresponding expression product, indicates an increased likelihood of positive clinical outcome. The prediction of clinical outcome may comprise an estimate of the likelihood of a particular clinical outcome for a subject or may comprise the classification of a subject into a risk group based on said estimate.

In another aspect the invention is directed to a report predicting clinical outcome in a subject diagnosed with Dukes C (stage III) colorectal cancer following surgical resection of said cancer, comprising a prediction of clinical outcome based on information comprising the expression level of one or more predictive RNA transcripts selected from the group consisting of CAPG, CD28, CKS1B, CYR61, DKK1, HSD17B2, LOX, MMP7, SIR2, ALCAM, CD24, CDC20, CDH11, CENPE, CLTC, EMR3, ICAM2, MADH2, MGAT5, MT3, NUFIP1, PRDX6, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, and WIF, or their expression products, in a biological sample comprising cancer cells obtained from said subject, wherein: (a) evidence of increased expression of one or more of the genes selected from the group consisting of CAPG, CD28, CKS1B, CYR61, DKK1, HSD17B2, LOX, MMP7, and SIR2, or the corresponding expression product, indicates a decreased likelihood of positive clinical outcome; and (b) evidence of increased expression of one or more of the genes selected from the group consisting of ALCAM, CD24, CDC20, CDH11, CENPE, CLTC, EMR3, ICAM2, MADH2, MGAT5, MT3, NUFIP1, PRDX6, SOS1, STAT5B, TFF3, TMSB4X, TP53BP1, and WIF, or the corresponding expression product, indicates an increased likelihood of positive clinical outcome. The prediction of clinical outcome may comprise an estimate of the likelihood of a particular clinical outcome for a subject or may comprise the classification of a subject into a risk group based on said estimate.

In a different aspect the invention concerns a kit comprising one or more of (1) extraction buffer/reagents and protocol; (2) reverse transcription buffer/reagents and protocol; and (3) qPCR buffer/reagents and protocol suitable for performing the methods of this invention. The kit may comprise data retrieval and analysis software.

BRIEF DESCRIPTION OF DRAWINGS

FIG. **1** shows a dendrogram representing the expression clustering of 142 genes that were statistically significantly related to recurrence-free interval (Tables 1.2A and 1.2B) in the univariate Cox proportional hazards analysis. The cluster analysis used the unweighted pair-group average amalgamation method and 1-Pearson r as the distance measure. The identities of particular genes in clusters of interest are indicated along the x-axis.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

A. Definitions

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton et al., Dictionary of Microbiology and Molecular Biology 2nd ed., J. Wiley & Sons (New York, N.Y. 1994), and March, Advanced Organic Chemistry Reactions, Mechanisms and Structure 4th ed., John Wiley & Sons (New York, N.Y. 1992), provide one skilled in the art with a general guide to many of the terms used in the present application.

One skilled in the art will recognize many methods and materials similar or equivalent to those described herein, which could be used in the practice of the present invention. Indeed, the present invention is in no way limited to the methods and materials described. For purposes of the present invention, the following terms are defined below.

The term "tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include, but are not limited to, breast cancer, ovarian cancer, colon cancer, lung cancer, prostate cancer, hepatocellular cancer, gastric cancer, pancreatic cancer, cervical cancer, liver cancer, bladder cancer, cancer of the urinary tract, thyroid cancer, renal cancer, carcinoma, melanoma, and brain cancer.

The "pathology" of cancer includes all phenomena that compromise the well-being of the patient. This includes, without limitation, abnormal or uncontrollable cell growth, metastasis, interference with the normal functioning of neighboring cells, release of cytokines or other secretory products at abnormal levels, suppression or aggravation of inflammatory or immunological response, neoplasia, premalignancy, malignancy, invasion of surrounding or distant tissues or organs, such as lymph nodes, etc.

The term "colorectal cancer" is used in the broadest sense and refers to (1) all stages and all forms of cancer arising from epithelial cells of the large intestine and/or rectum and/or (2) all stages and all forms of cancer affecting the lining of the large intestine and/or rectum. In the staging systems used for classification of colorectal cancer, the colon and rectum are treated as one organ.

According to the tumor, node, metastasis (TNM) staging system of the American Joint Committee on Cancer (AJCC) (Greene et al. (eds.), AJCC Cancer Staging Manual. 6th Ed. New York, N.Y.: Springer; 2002), the various stages of colorectal cancer are defined as follows:

Tumor: T1: tumor invades submucosa; T2: tumor invades muscularis propria; T3: tumor invades through the muscularis propria into the subserose, or into the pericolic or perirectal tissues; T4: tumor directly invades other organs or structures, and/or perforates.

Node: N0: no regional lymph node metastasis; N1: metastasis in 1 to 3 regional lymph nodes; N2: metastasis in 4 or more regional lymph nodes.

Metastasis: M0: mp distant metastasis; M1: distant metastasis present.

Stage groupings: Stage I: T1 N0 M0; T2 N0 M0; Stage II: T3 N0 M0; T4 N0 M0; Stage III: any T, N1-2; M0; Stage IV: any T, any N, M1.

According to the Modified Duke Staging System, the various stages of colorectal cancer are defined as follows:

Stage A: the tumor penetrates into the mucosa of the bowel wall but not further. Stage B: tumor penetrates into and through the muscularis propria of the bowel wall; Stage C: tumor penetrates into but not through muscularis propria of the bowel wall, there is pathologic evidence of colorectal cancer in the lymph nodes; or tumor penetrates into and through the muscularis propria of the bowel wall, there is pathologic evidence of cancer in the lymph nodes; Stage D: tumor has spread beyond the confines of the lymph nodes, into other organs, such as the liver, lung or bone.

Prognostic factors are those variables related to the natural history of colorectal cancer, which influence the recurrence rates and outcome of patients once they have developed colorectal cancer. Clinical parameters that have been associated with a worse prognosis include, for example, lymph node involvement, and high grade tumors. Prognostic factors are frequently used to categorize patients into subgroups with different baseline relapse risks.

The term "prognosis" is used herein to refer to the prediction of the likelihood of cancer-attributable death or progression, including recurrence, metastatic spread, and drug resistance, of a neoplastic disease, such as colon cancer.

The term "prediction" is used herein to refer to the likelihood that a patient will have a particular clinical outcome, whether positive or negative, following surgical removal of the primary tumor. The predictive methods of the present invention can be used clinically to make treatment decisions by choosing the most appropriate treatment modalities for any particular patient. The predictive methods of the present invention are valuable tools in predicting if a patient is likely to respond favorably to a treatment regimen, such as surgical intervention. The prediction may include prognostic factors.

The term "positive clinical outcome" means an improvement in any measure of patient status, including those measures ordinarily used in the art, such as an increase in the duration of Recurrence-Free interval (RFI), an increase in the time of Overall Survival (OS), an increase in the time of Disease-Free Survival (DFS), an increase in the duration of Distant Recurrence-Free Interval (DRFI), and the like. An increase in the likelihood of positive clinical outcome corresponds to a decrease in the likelihood of cancer recurrence.

The term "risk classification" means the level of risk or the prediction that a subject will experience a particular clinical outcome. A subject may be classified into a risk group or classified at a level of risk based on the predictive methods of the present invention. A "risk group" is a group of subjects or individuals with a similar level of risk for a particular clinical outcome.

The term "long-term" survival is used herein to refer to survival for at least 3 years, more preferably for at least 5 years.

The term "Recurrence-Free Interval (RFI)" is used herein to refer to time in years to first colon cancer recurrence censoring for second primary cancer as a first event or death without evidence of recurrence.

The term "Overall Survival (OS)" is used herein to refer to time in years from surgery to death from any cause.

The term "Disease-Free Survival (DFS)" is used herein to refer to time in years to colon cancer recurrence or death from any cause.

The term "Distant Recurrence-Free Interval (DRFI)" is used herein to refer to the time (in years) from surgery to the first anatomically distant cancer recurrence.

The calculation of the measures listed above in practice may vary from study to study depending on the definition of events to be either censored or not considered.

The term "microarray" refers to an ordered arrangement of hybridizable array elements, preferably polynucleotide probes, on a substrate.

The term "polynucleotide," when used in singular or plural, generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, polynucleotides as defined herein include, without limitation, single- and double-stranded DNA, DNA including single- and double-stranded regions, single- and double-stranded RNA, and RNA including single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or include single- and double-stranded regions. In addition, the term "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. The term "polynucleotide" specifically includes cDNAs. The term includes DNAs (including cDNAs) and RNAs that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritiated bases, are included within the term "polynucleotides" as defined herein. In general, the term "polynucleotide" embraces all chemically, enzymatically and/or metabolically modified forms of unmodified polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells.

The term "oligonucleotide" refers to a relatively short polynucleotide, including, without limitation, single-stranded deoxyribonucleotides, single- or double-stranded ribonucleotides, RNA:DNA hybrids and double-stranded DNAs. Oligonucleotides, such as single-stranded DNA probe oligonucleotides, are often synthesized by chemical methods, for example using automated oligonucleotide synthesizers that are commercially available. However, oligonucleotides can be made by a variety of other methods, including in vitro recombinant DNA-mediated techniques and by expression of DNAs in cells and organisms.

The terms "differentially expressed gene," "differential gene expression" and their synonyms, which are used interchangeably, refer to a gene whose expression is activated to a higher or lower level in a subject suffering from a disease, specifically cancer, such as colon cancer, relative to its expression in a normal or control subject. The terms also include genes whose expression is activated to a higher or lower level at different stages of the same disease. It is also understood that a differentially expressed gene may be either activated or inhibited at the nucleic acid level or protein level, or may be subject to alternative splicing to result in a different polypeptide product. Such differences may be evidenced by a change in mRNA levels, surface expression, secretion or other partitioning of a polypeptide, for example. Differential gene expression may include a comparison of expression between two or more genes or their gene products, or a comparison of the ratios of the expression between two or more genes or their gene products, or even a comparison of two differently processed products of the same gene, which differ between normal subjects and subjects suffering from a disease, specifically cancer, or between various stages of the same disease. Differential expression includes both quantitative, as well as qualitative, differences in the temporal or cellular expression pattern in a gene or its expression products among, for example, normal and diseased cells, or among cells which have undergone different disease events or disease stages. For the purpose of this invention, "differential gene expression" is considered to be present when there is at least an about two-fold, preferably at least about four-fold, more preferably at least about six-fold, most preferably at least about ten-fold difference between the expression of a given gene in normal and diseased subjects, or in various stages of disease development in a diseased subject.

The term "over-expression" with regard to an RNA transcript is used to refer to the level of the transcript determined by normalization to the level of reference mRNAs, which might be all measured transcripts in the specimen or a particular reference set of mRNAs.

The phrase "gene amplification" refers to a process by which multiple copies of a gene or gene fragment are formed in a particular cell or cell line. The duplicated region (a stretch of amplified DNA) is often referred to as "amplicon." Usually, the amount of the messenger RNA (mRNA) produced, i.e., the level of gene expression, also increases in the proportion of the number of copies made of the particular gene expressed.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., *Current Protocols in Molecular Biology*, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, typically: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50° C.; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42° C.; or (3) employ 50% formamide, 5×SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5×Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42° C., with washes at 42° C. in 0.2×SSC (sodium chloride/sodium citrate) and 50% formamide, followed by a high-stringency wash consisting of 0.1×SSC containing EDTA at 55° C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and % SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37° C. in a solution comprising: 20% formamide, 5×SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5×Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1×SSC at about 37-50° C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

In the context of the present invention, reference to "at least one," "at least two," "at least five," etc. of the genes listed in any particular gene set means any one or any and all combinations of the genes listed.

The term "node negative" cancer, such as "node negative" colon cancer, is used herein to refer to cancer that has not spread to the lymph nodes.

The terms "splicing" and "RNA splicing" are used interchangeably and refer to RNA processing that removes introns and joins exons to produce mature mRNA with continuous coding sequence that moves into the cytoplasm of an eukaryotic cell.

In theory, the term "exon" refers to any segment of an interrupted gene that is represented in the mature RNA product (B. Lewin. *Genes IV* Cell Press, Cambridge Mass. 1990). In theory the term "intron" refers to any segment of DNA that is transcribed but removed from within the transcript by splicing together the exons on either side of it. Operationally, exon sequences occur in the mRNA sequence of a gene as defined by Ref. SEQ ID numbers. Operationally, intron sequences are the intervening sequences within the genomic DNA of a gene, bracketed by exon sequences and having GT and AG splice consensus sequences at their 5' and 3' boundaries.

The term "expression cluster" is used herein to refer to a group of genes which demonstrate similar expression patterns when studied within samples from a defined set of patients. As used herein, the genes within an expression cluster show similar expression patterns when studied within samples from patients with Stage II and/or Stage III cancers of the colon and/or rectum.

B.1 General Description of the Invention

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, and biochemistry, which are within the skill of the art. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual", 2nd edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M. J. Gait, ed., 1984); "Animal Cell Culture" (R. I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Handbook of Experimental Immunology", 4th edition (D. M. Weir & C. C. Blackwell, eds., Blackwell Science Inc., 1987); "Gene Transfer Vectors for Mammalian Cells" (J. M. Miller & M. P. Calos, eds., 1987); "Current Protocols in Molecular Biology" (F. M. Ausubel et al., eds., 1987); and "PCR: The Polymerase Chain Reaction", (Mullis et al., eds., 1994).

Based on evidence of differential expression of RNA transcripts in normal and cancer cells, the present invention provides prognostic gene markers for colorectal cancer. Thus, in a particular aspect, the invention provides prognostic gene markers of Stage II and/or Stage III colorectal cancer, including markers that are specifically prognostic to the outcome of either Stage II or Stage III disease and those that have prognostic value at both stages, reflecting underlying differences in tumor cells in the two stages and/or in the extent of tumor progression. The prognostic markers and associated information provided by the present invention allow physicians to make more intelligent treatment decisions, and to customize the treatment of colorectal cancer to the needs of individual patients, thereby maximizing the benefit of treatment and minimizing the exposure of patients to unnecessary treatments, which do not provide any significant benefits and often carry serious risks due to toxic side-effects.

Disruptions in the normal functioning of various physiological processes, including proliferation, apoptosis, angiogenesis and invasion, have been implicated in the pathology in cancer. The relative contribution of dysfunctions in particular physiological processes to the pathology of particular cancer types is not well characterized. Any physiological process integrates the contributions of numerous gene products expressed by the various cells involved in the process. For example, tumor cell invasion of adjacent normal tissue and intravasation of the tumor cell into the circulatory system are effected by an array of proteins that mediate various cellular characteristics, including cohesion among tumor cells, adhesion of tumor cells to normal cells and connective tissue, ability of the tumor cell first to alter its morphology and then to migrate through surrounding tissues, and ability of the tumor cell to degrade surrounding connective tissue structures.

Multi-analyte gene expression tests can measure the expression level of one or more genes involved in each of several relevant physiologic processes or component cellular characteristics. In some instances the predictive power of the test, and therefore its utility, can be improved by using the expression values obtained for individual genes to calculate a score which is more highly correlated with outcome than is the expression value of the individual genes. For example, the calculation of a quantitative score (recurrence score) that predicts the likelihood of recurrence in estrogen receptor-positive, node-negative breast cancer is describe in a co-pending U.S. patent application (Publication Number 20050048542). The equation used to calculate such a recurrence score may group genes in order to maximize the predictive value of the recurrence score. The grouping of genes may be performed at least in part based on knowledge of their contribution to physiologic functions or component cellular characteristics such as discussed above. The formation of groups, in addition, can facilitate the mathematical weighting of the contribution of various expression values to the recurrence score. The weighting of a gene group representing a physiological process or component cellular characteristic can reflect the contribution of that process or characteristic to the pathology of the cancer and clinical outcome. Accordingly, in an important aspect, the present invention also provides specific groups of the prognostic genes identified herein, that together are more reliable and powerful predictors of outcome than the individual genes or random combinations of the genes identified.

In addition, based on the determination of a recurrence score, one can choose to partition patients into subgroups at any particular value(s) of the recurrence score, where all patients with values in a given range can be classified as belonging to a particular risk group. Thus, the values chosen will define subgroups of patients with respectively greater or lesser risk.

The utility of a gene marker in predicting colon cancer outcome may not be unique to that marker. An alternative marker having a expression pattern that is closely similar to a particular test marker may be substituted for or used in addition to a test marker and have little impact on the overall predictive utility of the test. The closely similar expression patterns of two genes may result from involvement of both genes in a particular process and/or being under common regulatory control in colon tumor cells. The present invention specifically includes and contemplates the use of such substitute genes or gene sets in the methods of the present invention.

The prognostic markers and associated information provided by the present invention predicting the clinical outcome in Stage II and/or Stage III cancers of the colon and/or rectum has utility in the development of drugs to treat Stage II and/or Stage III cancers of the colon and/or rectum.

The prognostic markers and associated information provided by the present invention predicting the clinical outcome in Stage II and/or Stage III cancers of the colon and/or rectum also have utility in screening patients for inclusion in clinical trials that test the efficacy of drug compounds for the treatment of patients with Stage II and/or Stage III cancers of the colon and/or rectum. In particular the prognostic markers may be used on samples collected from patients in a clinical trial and the results of the test used in conjunction with patient outcomes in order to determine whether subgroups of patients are more or less likely to show a response to the drug than the whole group or other subgroups.

The prognostic markers and associated information provided by the present invention predicting the clinical outcome in Stage II and/or Stage III cancers of the colon and/or rectum are useful as inclusion criterion for a clinical trial. For example, a patient is more likely to be included in a clinical trial if the results of the test indicate a higher likelihood that the patient will have a poor clinical outcome if treated with surgery alone and a patient is less likely to be included in a clinical trial if the results of the test indicate a lower likelihood that the patient will have a poor clinical outcome if treated with surgery alone.

In a particular embodiment, prognostic markers and associated information are used to design or produce a reagent that modulates the level or activity of the gene's transcript or its expression product. Said reagents may include but are not limited to an antisense RNA, a small inhibitory RNA, a ribozyme, a monoclonal or polyclonal antibody.

In a further embodiment, said gene or its transcript, or more particularly, an expression product of said transcript is used in an (screening) assay to identify a drug compound, wherein said drug compounds is used in the development of a drug to treat Stage II and/or Stage III cancers of the colon and/or rectum.

In various embodiments of the inventions, various technological approaches are available for determination of expression levels of the disclosed genes, including, without limitation, RT-PCR, microarrays, serial analysis of gene expression (SAGE) and Gene Expression Analysis by Massively Parallel Signature Sequencing (MPSS), which will be discussed in detail below. In particular embodiments, the expression level of each gene may be determined in relation to various features of the expression products of the gene including exons, introns, protein epitopes and protein activity. In other embodiments, the expression level of a gene may be inferred from analysis of the structure of the gene, for example from the analysis of the methylation pattern of gene's promoter(s).

B.2 Gene Expression Profiling

Methods of gene expression profiling include methods based on hybridization analysis of polynucleotides, methods based on sequencing of polynucleotides, and proteomics-based methods. The most commonly used methods known in the art for the quantification of mRNA expression in a sample include northern blotting and in situ hybridization (Parker & Barnes, Methods in Molecular Biology 106:247-283 (1999)); RNAse protection assays (Hod, Biotechniques 13:852-854 (1992)); and PCR-based methods, such as reverse transcription polymerase chain reaction (RT-PCR) (Weis et al., Trends in Genetics 8:263-264 (1992)). Alternatively, antibodies may be employed that can recognize sequence-specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. Representative methods for sequencing-based gene expression analysis include Serial Analysis of Gene Expression (SAGE), and gene expression analysis by massively parallel signature sequencing (MPSS).

a. Reverse Transcriptase PCR (RT-PCR)

Of the techniques listed above, the most sensitive and most flexible quantitative method is RT-PCR, which can be used to determine mRNA levels in various samples. The results can be used to compare gene expression patterns between sample sets, for example in normal and tumor tissues and in patients with or without drug treatment.

The first step is the isolation of mRNA from a target sample. The starting material is typically total RNA isolated from human tumors or tumor cell lines, and corresponding normal tissues or cell lines, respectively. Thus RNA can be isolated from a variety of primary tumors, including breast, lung, colon, prostate, brain, liver, kidney, pancreas, spleen, thymus, testis, ovary, uterus, etc., tumor, or tumor cell lines, with pooled DNA from healthy donors. If the source of mRNA is a primary tumor, mRNA can be extracted, for example, from frozen or archived paraffin-embedded and fixed (e.g. formalin-fixed) tissue samples.

General methods for mRNA extraction are well known in the art and are disclosed in standard textbooks of molecular biology, including Ausubel et al., *Current Protocols of Molecular Biology*, John Wiley and Sons (1997). Methods for RNA extraction from paraffin embedded tissues are disclosed, for example, in Rupp and Locker, *Lab Invest.* 56:A67 (1987), and De Andrés et al., *BioTechniques* 18:42044 (1995). In particular, RNA isolation can be performed using purification kit, buffer set and protease from commercial manufacturers, such as Qiagen, according to the manufacturer's instructions. For example, total RNA from cells in culture can be isolated using Qiagen RNeasy mini-columns. Other commercially available RNA isolation kits include MasterPure™ Complete DNA and RNA Purification Kit (EPICENTRE®, Madison, Wis.), and Paraffin Block RNA Isolation Kit (Ambion, Inc.). Total RNA from tissue samples can be isolated using RNA Stat-60 (Tel-Test). RNA prepared from tumor can be isolated, for example, by cesium chloride density gradient centrifugation.

As RNA cannot serve as a template for PCR, the first step in gene expression profiling by RT-PCR is the reverse transcription of the RNA template into cDNA, followed by its exponential amplification in a PCR reaction. The two most commonly used reverse transcriptases are avilo myeloblastosis virus reverse transcriptase (AMV-RT) and Moloney murine leukemia virus reverse transcriptase (MMLV-RT). The reverse transcription step is typically primed using specific primers, random hexamers, or oligo-dT primers, depending on the circumstances and the goal of expression profiling. For example, extracted RNA can be reverse-transcribed using a GeneAmp RNA PCR kit (Perkin Elmer, CA, USA), following the manufacturer's instructions. The derived cDNA can then be used as a template in the subsequent PCR reaction.

Although the PCR step can use a variety of thermostable DNA-dependent DNA polymerases, it typically employs the Taq DNA polymerase, which has a 5'-3' nuclease activity but lacks a 3'-5' proofreading endonuclease activity. Thus, TaqMan® PCR typically utilizes the 5'-nuclease activity of Taq or Tth polymerase to hydrolyze a hybridization probe bound to its target amplicon, but any enzyme with equivalent 5' nuclease activity can be used. Two oligonucleotide primers are used to generate an amplicon typical of a PCR reaction. A third oligonucleotide, or probe, is designed to detect nucleotide sequence located between the two PCR primers. The probe is non-extendible by Taq DNA polymerase enzyme, and is labeled with a reporter fluorescent dye and a quencher fluorescent dye. Any laser-induced emission from the reporter dye is quenched by the quenching dye when the two dyes are located close together as they are on the probe. During the amplification reaction, the Taq DNA polymerase enzyme cleaves the probe in a template-dependent manner. The resultant probe fragments disassociate in solution, and signal from the released reporter dye is free from the quenching effect of the second fluorophore. One molecule of reporter dye is liberated for each new molecule synthesized, and detection of the unquenched reporter dye provides the basis for quantitative interpretation of the data.

TaqMan® RT-PCR can be performed using commercially available equipment, such as, for example, ABI PRISM 7700™ Sequence Detection System™ (Perkin-Elmer-Applied Biosystems, Foster City, Calif., USA), or Lightcycler (Roche Molecular Biochemicals, Mannheim, Germany). In a preferred embodiment, the 5' nuclease procedure is run on a real-time quantitative PCR device such as the ABI PRISM 7700™ Sequence Detection System™. The system consists of a thermocycler, laser, charge-coupled device (CCD), camera and computer. The system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and detected at the CCD. The system includes software for running the instrument and for analyzing the data.

5'-Nuclease assay data are initially expressed as Ct, or the threshold cycle. As discussed above, fluorescence values are recorded during every cycle and represent the amount of product amplified to that point in the amplification reaction. The point when the fluorescent signal is first recorded as statistically significant is the threshold cycle (C_t).

To minimize errors and the effect of sample-to-sample variation, RT-PCR is usually performed using an internal standard. The ideal internal standard is expressed at a constant level among different tissues, and is unaffected by the experimental treatment. RNAs most frequently used to normalize patterns of gene expression are mRNAs for the housekeeping genes glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) and β-actin.

A more recent variation of the RT-PCR technique is the real time quantitative PCR, which measures PCR product accumulation through a dual-labeled fluorigenic probe (i.e., TaqMan® probe). Real time PCR is compatible both with quantitative competitive PCR, where internal competitor for each target sequence is used for normalization, and with quantitative comparative PCR using a normalization gene contained within the sample, or a housekeeping gene for RT-PCR. For further details see, e.g. Held et al., *Genome Research* 6:986-994 (1996).

The steps of a representative protocol for profiling gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA isolation, purification, primer extension and amplification are given in various published journal articles (for example: T. E. Godfrey et al. J. Molec. Diagnostics 2: 84-91 (2000); K. Specht et al., Am. J. Pathol. 158: 419-29 (2001)). Briefly, a representative process starts with cutting about 10 μm thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA are removed. After analysis of the RNA concentration, RNA repair and/or amplification steps may be included, if necessary, and RNA is reverse transcribed using gene specific promoters followed by RT-PCR.

b. MassARRAY System

In the MassARRAY-based gene expression profiling method, developed by Sequenom, Inc. (San Diego, Calif.) following the isolation of RNA and reverse transcription, the obtained cDNA is spiked with a synthetic DNA molecule (competitor), which matches the targeted cDNA region in all positions, except a single base, and serves as an internal standard. The cDNA/competitor mixture is PCR amplified and is subjected to a post-PCR shrimp alkaline phosphatase (SAP) enzyme treatment, which results in the dephosphorylation of the remaining nucleotides. After inactivation of the alkaline phosphatase, the PCR products from the competitor and cDNA are subjected to primer extension, which generates distinct mass signals for the competitor- and cDNA-derives PCR products. After purification, these products are dispensed on a chip array, which is pre-loaded with components needed for analysis with matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) analysis. The cDNA present in the reaction is then quantified by analyzing the ratios of the peak areas in the mass spectrum generated. For further details see, e.g. Ding and Cantor, Proc. Natl. Acad. Sci. USA 100:3059-3064 (2003).

c. Other PCR-Based Methods

Further PCR-based techniques include, for example, differential display (Liang and Pardee, Science 257:967-971 (1992)); amplified fragment length polymorphism (iAFLP) (Kawamoto et al., Genome Res. 12:1305-1312 (1999)); BeadArray™ technology (Illumina, San Diego, Calif.; Oliphant et al., Discovery of Markers for Disease (Supplement to Biotechniques), June 2002; Ferguson et al., Analytical Chemistry 72:5618 (2000)); BeadsArray for Detection of Gene Expression (BADGE), using the commercially available Luminex100 LabMAP system and multiple color-coded microspheres (Luminex Corp., Austin, Tex.) in a rapid assay for gene expression (Yang et al., Genome Res. 11:1888-1898 (2001)); and high coverage expression profiling (HiCEP) analysis (Fukumura et al., Nucl. Acids. Res. 31(16) e94 (2003)).

d. Microarrays

Differential gene expression can also be identified, or confirmed using the microarray technique. Thus, the expression profile of colon cancer-associated genes can be measured in either fresh or paraffin-embedded tumor tissue, using microarray technology. In this method, polynucleotide sequences of interest (including cDNAs and oligonucleotides) are plated, or arrayed, on a microchip substrate. The arrayed sequences are then hybridized with specific DNA probes from cells or tissues of interest. Just as in the RT-PCR method, the source of mRNA typically is total RNA isolated from human tumors or tumor cell lines, and corresponding normal tissues or cell lines. Thus RNA can be isolated from a variety of primary tumors or tumor cell lines. If the source of mRNA is a primary tumor, mRNA can be extracted, for example, from frozen or archived paraffin-embedded and fixed (e.g. formalin-fixed) tissue samples, which are routinely prepared and preserved in everyday clinical practice.

In a specific embodiment of the microarray technique, PCR amplified inserts of cDNA clones are applied to a substrate in a dense array. Preferably at least 10,000 nucleotide sequences are applied to the substrate. The microarrayed genes, immobilized on the microchip at 10,000 elements each, are suitable for hybridization under stringent conditions. Fluorescently labeled cDNA probes may be generated through incorporation of fluorescent nucleotides by reverse transcription of RNA extracted from tissues of interest. Labeled cDNA probes applied to the chip hybridize with specificity to each spot of DNA on the array. After stringent washing to remove non-specifically bound probes, the chip is scanned by confocal laser microscopy or by another detection method, such as a CCD camera. Quantitation of hybridization of each arrayed element allows for assessment of corresponding mRNA abundance. With dual color fluorescence, separately labeled cDNA probes generated from two sources of RNA are hybridized pair wise to the array. The relative abundance of the transcripts from the two sources corresponding to each specified gene is thus determined simultaneously. The miniaturized scale of the hybridization affords a convenient and rapid evaluation of the expression pattern for large numbers of genes. Such methods have been shown to have the sensitivity required to detect rare transcripts, which are expressed at a few copies per cell, and to reproducibly detect at least approximately two-fold differences in the expression levels (Schena et al., *Proc. Natl. Acad. Sci. USA* 93(2):106-149 (1996)). Microarray analysis can be performed by commercially available equipment, following manufacturer's protocols, such as by using the Affymetrix GenChip technology, or Incyte's microarray technology.

The development of microarray methods for large-scale analysis of gene expression makes it possible to search systematically for molecular markers of cancer classification and outcome prediction in a variety of tumor types.

e. Serial Analysis of Gene Expression (SAGE)

Serial analysis of gene expression (SAGE) is a method that allows the simultaneous and quantitative analysis of a large number of gene transcripts, without the need of providing an individual hybridization probe for each transcript. First, a short sequence tag (about 10-14 bp) is generated that contains sufficient information to uniquely identify a transcript, provided that the tag is obtained from a unique position within each transcript. Then, many transcripts are linked together to form long serial molecules, that can be sequenced, revealing the identity of the multiple tags simultaneously. The expression pattern of any population of transcripts can be quantitatively evaluated by determining the abundance of individual tags, and identifying the gene corresponding to each tag. For more details see, e.g. Velculescu et al., *Science* 270:484-487 (1995); and Velculescu et al., *Cell* 88:243-51 (1997).

f. Gene Expression Analysis by Massively Parallel Signature Sequencing (MPSS)

This method, described by Brenner et al., *Nature Biotechnology* 18:630-634 (2000), is a sequencing approach that combines non-gel-based signature sequencing with in vitro cloning of millions of templates on separate 5 μm diameter microbeads. First, a microbead library of DNA templates is constructed by in vitro cloning. This is followed by the assembly of a planar array of the template-containing microbeads in a flow cell at a high density (typically greater than 3×10^6 microbeads/cm^2). The free ends of the cloned templates on each microbead are analyzed simultaneously, using a fluorescence-based signature sequencing method that does not require DNA fragment separation. This method has been shown to simultaneously and accurately provide, in a single operation, hundreds of thousands of gene signature sequences from a yeast cDNA library.

g. Immunohistochemistry

Immunohistochemistry methods are also suitable for detecting the expression levels of the prognostic markers of the present invention. Thus, antibodies or antisera, preferably polyclonal antisera, and most preferably monoclonal antibodies specific for each marker are used to detect expression. The antibodies can be detected by direct labeling of the antibodies themselves, for example, with radioactive labels, fluorescent labels, hapten labels such as, biotin, or an enzyme such as horse radish peroxidase or alkaline phosphatase.

Alternatively, unlabeled primary antibody is used in conjunction with a labeled secondary antibody, comprising antisera, polyclonal antisera or a monoclonal antibody specific for the primary antibody. Immunohistochemistry protocols and kits are well known in the art and are commercially available.

h. Proteomics

The term "proteome" is defined as the totality of the proteins present in a sample (e.g. tissue, organism, or cell culture) at a certain point of time. Proteomics includes, among other things, study of the global changes of protein expression in a sample (also referred to as "expression proteomics"). Proteomics typically includes the following steps: (1) separation of individual proteins in a sample by 2-D gel electrophoresis (2-D PAGE); (2) identification of the individual proteins recovered from the gel, e.g. my mass spectrometry or N-terminal sequencing, and (3) analysis of the data using bioinformatics. Proteomics methods are valuable supplements to other methods of gene expression profiling, and can be used, alone or in combination with other methods, to detect the products of the prognostic markers of the present invention.

i. Promoter Methylation Analysis

A number of methods for quantization of RNA transcripts (gene expression analysis) or their protein translation products are discussed herein. The expression level of genes may also be inferred from information regarding chromatin structure, such as for example the methylation status of gene promoters and other regulatory elements and the acetylation status of histones.

In particular, the methylation status of a promoter influences the level of expression of the gene regulated by that promoter. Aberrant methylation of particular gene promoters has been implicated in expression regulation, such as for example silencing of tumor suppressor genes. Thus, examination of the methylation status of a gene's promoter can be utilized as a surrogate for direct quantization of RNA levels.

Several approaches for measuring the methylation status of particular DNA elements have been devised, including methylation-specific PCR (Herman J. G. et al. (1996) Methylation-specific PCR: a novel PCR assay for methylation status of CpG islands. Proc. Natl Acad. Sci. USA. 93, 9821-9826.) and bisulfite DNA sequencing (Frommer M. et al. (1992) A genomic sequencing protocol that yields a positive display of 5-methylcytosine residues in individual DNA strands. Proc. Natl Acad. Sci. USA. 89, 1827-1831.). More recently, microarray-based technologies have been used to characterize promoter methylation status (Chen C. M. (2003) Methylation target array for rapid analysis of CpG island hypermethylation in multiple tissue genomes. Am. J. Pathol. 163, 3745.).

j. Coexpression of Genes

A further aspect of the invention is the identification of gene expression clusters. Gene expression clusters can be identified by analysis of expression data using statistical analyses known in the art, including pairwise analysis of correlation based on Pearson correlation coefficients (Pearson K. and Lee A. (1902) *Biometrika* 2, 357).

In one embodiment, an expression cluster identified herein includes BGN, CALD1, COL1A1, COL1A2, SPARC, VIM and other genes which are known to be synthesized predominantly by stromal cells and to be involved in remodeling extracellular matrix. This expression cluster is referred to herein as the Extracellular Matrix Remodeling/Stromal cluster.

In another embodiment, an expression cluster identified herein includes ANXA2, KLK6, KLK10, LAMA3, LAMC2, MASPIN, SLPI, and other genes encoding epithelial cell secreted products, most of which are secreted predominantly by epithelial cells but which may be secreted by other cell types. This expression cluster is referred to herein as the Epithelial/Secreted cluster.

In still another embodiment, an expression cluster identified herein includes DUSP1, EGR1, EGR3, FOS, NR4A1, RHOB, and other genes whose transcription is upregulated early after exposure of cells to certain stimuli. A variety of stimuli trigger transcription of early response genes, e.g. exposure to growth factor s, which enables cells to quickly increase their motility and their ability to transport nutrients such as glucose. This expression cluster is referred to herein as the Early Response cluster.

In yet another embodiment, an expression cluster identified herein includes MCP1, CD68, CTSB, OPN, and other genes encoding proteins usually associated with cells of the immune system. This expression cluster is referred to herein as the Immune cluster.

In a further embodiment, an expression cluster identified herein includes CCNE2, CDC20, SKP2, CHK1, BRCA1, CSEL1 and other genes implicated in cell proliferation and regulation of the cell cycle. This expression cluster is referred to herein as the Proliferation/Cell Cycle cluster.

k. General Description of the mRNA Isolation, Purification and Amplification

The steps of a representative protocol for profiling gene expression using fixed, paraffin-embedded tissues as the RNA source, including mRNA isolation, purification, primer extension and amplification are provided in various published journal articles (for example: T. E. Godfrey et al., *J. Molec. Diagnostics* 2: 84-91 (2000); K. Specht et al., *Am. J. Pathol.* 158: 419-29 (2001)). Briefly, a representative process starts with cutting about 10 μm thick sections of paraffin-embedded tumor tissue samples. The RNA is then extracted, and protein and DNA are removed. After analysis of the RNA concentration, RNA repair and/or amplification steps may be included, if necessary, and RNA is reverse transcribed using gene specific promoters followed by RT-PCR. Finally, the data are analyzed to identify the best treatment option(s) available to the patient on the basis of the characteristic gene expression pattern identified in the tumor sample examined, dependent on the predicted likelihood of cancer recurrence.

l. Colon Cancer Gene Set, Assayed Gene Subsequences, and Clinical Application of Gene Expression Data

An important aspect of the present invention is to use the measured expression of certain genes by colon cancer tissue to provide prognostic information. For this purpose it is necessary to correct for (normalize away) both differences in the amount of RNA assayed and variability in the quality of the RNA used. Therefore, the assay typically measures and incorporates the expression of certain normalizing genes, including well known housekeeping genes, such as GAPDH and Cyp1. Alternatively, normalization can be based on the mean or median signal (Ct) of all of the assayed genes or a large subset thereof (global normalization approach). On a gene-by-gene basis, measured normalized amount of a patient tumor mRNA is compared to the amount found in a colon cancer tissue reference set. The number (N) of colon cancer tissues in this reference set should be sufficiently high to ensure that different reference sets (as a whole) behave essentially the same way. If this condition is met, the identity of the individual colon cancer tissues present in a particular set will have no significant impact on the relative amounts of the genes assayed. Usually, the colon cancer tissue reference set consists of at least about 30, preferably at least about 40 different FPE colon cancer tissue specimens. Unless noted otherwise, normalized expression levels for each mRNA/tested tumor/patient will be expressed as a percentage of the expression level measured in the reference set. More specifically, the reference set of a sufficiently high number (e.g. 40) of tumors yields a distribution of normalized levels of each mRNA species. The level measured in a particular tumor sample to be analyzed falls at some percentile within this range, which can be determined by methods well known in the art. Below, unless noted otherwise, reference to expression levels of a gene assume normalized expression relative to the reference set although this is not always explicitly stated.

m. Design of Intron-Based PCR Primers and Probes

According to one aspect of the present invention, PCR primers and probes are designed based upon intron sequences present in the gene to be amplified. Accordingly, the first step in the primer/probe design is the delineation of intron sequences within the genes. This can be done by publicly available software, such as the DNA BLAT software developed by Kent, W. J., *Genome Res.* 12(4):656-64 (2002), or by the BLAST software including its variations. Subsequent steps follow well established methods of PCR primer and probe design.

In order to avoid non-specific signals, it is important to mask repetitive sequences within the introns when designing the primers and probes. This can be easily accomplished by using the Repeat Masker program available on-line through the Baylor College of Medicine, which screens DNA sequences against a library of repetitive elements and returns a query sequence in which the repetitive elements are masked. The masked intron sequences can then be used to design primer and probe sequences using any commercially or otherwise publicly available primer/probe design packages, such as Primer Express (Applied Biosystems); MGB assay-by-design (Applied Biosystems); Primer3 (Steve Rozen and Helen J. Skaletsky (2000) Primer3 on the WWW for general users and for biologist programmers. In: Krawetz S, Misener S (eds) *Bioinformatics Methods and Protocols: Methods in Molecular Biology*. Humana Press, Totowa, N.J., pp 365-386).

The most important factors considered in PCR primer design include primer length, melting temperature (Tm), and G/C content, specificity, complementary primer sequences, and 3'-end sequence. In general, optimal PCR primers are generally 17-30 bases in length, and contain about 20-80%, such as, for example, about 50-60% G+C bases. Tm's between 50 and 80° C., e.g. about 50 to 70° C. are typically preferred.

For further guidelines for PCR primer and probe design see, e.g. Dieffenbach, C. W. et al., "General Concepts for PCR Primer Design" in: *PCR Primer, A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York, 1995, pp. 133-155; Innis and Gelfand, "Optimization of PCRs" in: *PCR Protocols, A Guide to Methods and Applications*, CRC Press, London, 1994, pp. 5-11; and Plasterer, T. N. Primerselect: Primer and probe design. *Methods Mol. Biol.* 70:520-527 (1997), the entire disclosures of which are hereby expressly incorporated by reference.

n. Kits of the Invention

The materials for use in the methods of the present invention are suited for preparation of kits produced in accordance with well known procedures. The invention thus provides kits comprising agents, which may include gene-specific or gene-selective probes and/or primers, for quantitating the expression of the disclosed genes for predicting prognostic outcome or response to treatment. Such kits may optionally contain reagents for the extraction of RNA from tumor samples, in particular fixed paraffin-embedded tissue samples and/or reagents for RNA amplification. In addition, the kits may optionally comprise the reagent(s) with an identifying description or label or instructions relating to their use in the methods of the present invention. The kits may comprise containers (including microtiter plates suitable for use in an automated implementation of the method), each with one or more of the various reagents (typically in concentrated form) utilized in the methods, including, for example, pre-fabricated microarrays, buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP, dGTP and dTTP; or rATP, rCTP, rGTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more probes and primers of the present invention (e.g., appropriate length poly(T) or random primers linked to a promoter reactive with the RNA polymerase). Mathematical algorithms used to estimate or quantify prognostic or predictive information are also properly potential components of kits.

o. Reports of the Invention

The methods of this invention, when practiced for commercial diagnostic purposes generally produce a report or summary of the normalized expression levels of one or more of the selected genes. The methods of this invention will produce a report comprising a prediction of the clinical outcome of a subject diagnosed with colorectal cancer following surgical resection of said cancer. The methods and reports of this invention can further include storing the report in a database. Alternatively, the method can further create a record in a database for the subject and populate the record with data. In one embodiment the report is a paper report, in another embodiment the report is an auditory report, in another embodiment the report is an electronic record. It is contemplated that the report is provided to a physician and/of the patient. The receiving of the report can further include establishing a network connection to a server computer that includes the data and report and requesting the data and report from the server computer.

The methods provided by the present invention may also be automated in whole or in part.

All aspects of the present invention may also be practiced such that a limited number of additional genes that are co-expressed with the disclosed genes, for example as evidenced by high Pearson correlation coefficients, are included in a prognostic or predictive test in addition to and/or in place of disclosed genes.

Having described the invention, the same will be more readily understood through reference to the following Example, which is provided by way of illustration, and is not intended to limit the invention in any way.

EXAMPLES

A Study to Explore Relationships Between Genomic Tumor Expression Profiles and the Likelihood of Recurrence in Dukes' B and Duke's C Patients Treated with Resection of the Colon

The primary objective of this study was to determine whether there is a significant relationship between the expression of each of 757 amplicons identified in Table B and clinical outcome in stage II and stage III colon cancer patients who receive colon resection (surgery) without chemotherapy.

Study Design

This was an exploratory study using tissue and outcome data from National Surgical Adjuvant Breast and Bowel Project (NSABP) Studies C-01 and C-02 in up to 400 Dukes B (stage II) and Dukes C (stage III) patients who received colon resection (surgery) only or surgery and postoperative Bacillus Calmette-Guerin (BCG).

Inclusion Criteria

Patients enrolled in either NSABP Study C-01: "A Clinical Trial To Evaluate Postoperative Immunotherapy And Postoperative Systemic Chemotherapy In The Management Of Resectable Colon Cancer" or NSABP Study C-02: "A Protocol To Evaluate The Postoperative Portal Vein Infusion Of 5-Flourouracil And Heparin In Adenocarcinoma Of The Colon" Details of C-01 and C-02 can be found on the NSABP Website at the following URL:

http://www.nsabp.pitt.edu/NSABP_Protocols.htm#treatment%20closed

Tissue samples from the surgery only and surgery+postoperative BCG arms of NSABP C01 and from the surgery only arm of NSABP C02 surgery were combined into one sample set.

Exclusion Criteria

Patients enrolled in NSABP Study C-01 or NSABP Study C-02 were excluded from the present study if one or more of the following applied:

No tumor block available from initial diagnosis in the NSABP archive.

Insufficient tumor in block as assessed by examination of hematoxylin and eosin (H&E) slide

Insufficient RNA (<700 ng) recovered from tissue sections for RT-PCR analysis.

Of 1943 patients enrolled in NSABP Study C-01 or NSABP Study C-02, 270 patient samples were available after application of exclusion criteria and used in the gene expression study disclosed herein. The overall demographic and clinical characteristics of the 270 included samples were similar to the original NSABP combined cohorts.

Gene Panel

Seven hundred sixty-one genes, including seven reference genes, were chosen for expression analysis. These genes are listed in Table A together with the sequences of primers and probes used in qRT-PCR to determine expression level.

Experimental Materials and Methods

The expression of 750 cancer-related genes and 7 genes designated for use as reference genes was quantitatively assessed for each patient using TaqMan® RT-PCR, which was performed in singlet with RNA input at 1 nanogram per reaction.

Data Analysis Methods

Reference Normalization

For normalization of extraneous effects, cycle threshold (C_T) measurements obtained by RT-PCR were normalized relative to the mean expression of a set of six reference genes. The resulting reference-normalized expression measurements typically range from 0 to 15, where a one unit increase generally reflects a 2-fold increase in RNA quantity.

Comparison of Study Cohort to Original NSABP Study Populations

We compared the distribution of clinical and demographic variables for the current study cohort of evaluable tissue blocks versus the original NSABP C-01 and C-02 study populations. There were no clinically meaningful differences in the distributions.

Univariate Analysis

For each of the 757 amplicons under study, we used the Cox proportional hazard model to examine the relationship between gene expression and recurrence free interval (RFI). The likelihood ratio was used as the test of statistical significance. The method of Benjamini and Hochberg (Benjamini, Y. and Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. J.R. Statist. Soc. B 57, 289-300.), as well as resampling and permutation based methods (Tusher V G, Tibshirani R, Chu G (2001) Significance analysis of microarrays applied to the ionizing radiation response. Proc Natl Acad Sci USA, 98:5116-5121; Storey J D, Tibshirani R (2001) Estimating false discovery rates under dependence, with applications to DNA microarrays. Stanford: Stanford University, Department of Statistics; Report No.: Technical Report 2001-28; Korn E L, Troendle J, McShane L, Simon R (2001) Controlling the number of false discoveries: Application to high-dimensional genomic data. Technical Report 003. 2001. National Cancer Institute.) were applied to the resulting set of p-values to estimate false discovery rates. All analyses were repeated for each of the alternative endpoints: distant recurrence free interval (DRFI), overall survival (OS), and disease free survival (DFS).

Multivariate Analysis

For each of the 757 amplicons under study, we used the Cox proportional hazard model to examine the relationship between gene expression and RFI, while controlling for the effects of other standard clinical covariates (including tumor location, surgery type, tumor grade, number of lymph nodes examined, and number of positive lymph nodes. The difference in the log likelihoods of the (reduced) model including only the standard clinical covariates and the (full) model including the standard clinical covariates plus gene expression was used as the test of statistical significance.

Non-Linear Analysis

For each of the 757 amplicons under study, we explored alternative functional relationships between gene expression and recurrence using several different methods. For each amplicon, we fit a Cox proportional hazards model of RFI as a function of gene expression using a 2 degree-of-freedom (DF) natural spline (Stone C, Koo C. (1985) In Proceedings of the Statistical Computing Section ASA. Washington, D.C., 45-48). Statistical significance was assessed by the 2 DF likelihood ratio test for the model. Functional relationships were also explored by examining the pattern of (smoothed) Martingale residuals derived from univariate Cox proportional hazards models of RFI as a strictly linear function of gene expression (Gray R J (1992) Flexible methods for analyzing survival data using splines, with applications to breast cancer prognosis. Journal of the American Statistical Association, 87:942-951; Gray R J (1994) Spline-based tests in survival analysis. Biometrics, 50:640-652; Gray R J (1990) Some diagnostic methods for Cox regression models through hazard smoothing. Biometrics, 46:93-102.). Additionally, cumulative sums of Martingale residuals from each the same Cox proportional hazards models were used to detect departures from linearity (Lin D, Wei L, Ying Z. (1993) Checking the Cox Model with Cumulative Sums of Martingale-Based Residuals. Vol. 80, No. 3, 557-572).

Interaction with Stage

We determined whether there is a significantly different relationship between gene expression and RFI in stage II and stage III patients. For each of the 757 amplicons, we tested the hypothesis that there is a significant difference between the (reduced) proportional hazards model for gene expression and tumor stage versus the (full) proportional hazards model based on gene expression, tumor stage, and their interaction. The difference in the log likelihoods of the reduced and full models was used as the test of statistical significance.

Table A shows qRT-PCR probe and primer sequences for all genes included in the study described in the Example.

Table B shows target amplicons for all genes included in the study described in the Example.

First Analysis Study Results

Reference Gene set for the first analysis was CLTC, FZD6, NEDD8, RPLPO, RPS13, UBB, UBC.

Table 1A shows associations for those genes whose increased expression is predictive of shorter Recurrence-Free Interval (RFI) based on univariate proportional hazards analysis.

Table 1B shows associations for those genes whose increased expression is predictive of longer Recurrence-Free Interval (RFI) based on univariate proportional hazards analysis.

Table 2A shows associations for those genes whose increased expression is predictive of decreased rate of Overall Survival (OS) based on univariate proportional hazards analysis.

Table 2B shows associations for those genes whose increased expression is predictive of increased rate of Overall Survival (OS) based on univariate proportional hazards analysis.

Table 3A shows associations for those genes whose increased expression is predictive of decreased rate of Disease Free Survival (DFS) based on univariate proportional hazards analysis.

Table 3B shows associations for those genes whose increased expression is predictive of increased rate of Disease Free Survival (DFS) based on univariate proportional hazards analysis.

Table 4A shows associations for those genes whose increased expression is predictive of shorter Distant Recurrence-Free Interval (DRFI) based on univariate proportional hazards analysis.

Table 4B shows associations for those genes whose increased expression is predictive of longer Distant Recurrence-Free Interval (DRFI) based on univariate proportional hazards analysis.

Table 5A shows associations between gene expression and RFI for those genes whose increased expression is predictive of shorter Recurrence-Free Interval (RFI), based on a multivariate analysis controlling for particular demographic and clinical characteristics of patients included in the analysis.

Table 5B shows associations between gene expression and RFI for those genes whose increased expression is predictive of longer Recurrence-Free Interval (RFI), based on a multivariate analysis controlling for particular demographic and clinical characteristics of patients included in the analysis.

Table 6 shows genes for which an association between gene expression and clinical outcome was identified based on a nonlinear proportional hazards analysis, using a 2 degree-of-freedom natural spline.

Table 7 shows all genes exhibiting an interaction (p-value<0.05) with tumor stage.

Table 1A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which $p<0.1$. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using RFI as the metric for clinical outcome.

TABLE 1A

Gene	Hazard Ratio	P Value	OfficialSymbol	Accession Number
RARB	2.13	0.0252	RARB	NM_016152
ITGB1	1.94	0.0002	ITGB1	NM_002211
ALDOA	1.92	0.0853	ALDOA	NM_000034
ANXA2	1.90	<.0001	ANXA2	NM_004039
CYP3A4	1.81	0.0038	CYP3A4	NM_017460
KRAS2	1.64	0.0043	KRAS	NM_004985
COX2	1.62	0.0521	PTGS2	NM_000963
RhoC	1.61	0.0034	RHOC	NM_175744
TJP1	1.60	0.0554	TJP1	NM_003257
RhoB	1.57	0.0001	RHOB	NM_004040
KIAA0125	1.56	0.0940	KIAA0125	NM_014792
TIMP1	1.52	<.0001	TIMP1	NM_003254
UBC	1.49	0.0031	UBC	NM_021009
ANXA5	1.49	0.0084	ANXA5	NM_001154
NTN1	1.49	0.0386	NTN1	NM_004822
AKT3	1.47	<.0001	AKT3	NM_005465
CALD1	1.46	0.0007	CALD1	NM_004342
IGFBP7	1.46	0.0019	IGFBP7	NM_001553
VEGFC	1.45	0.0092	VEGFC	NM_005429
BGN	1.44	0.0002	BGN	NM_001711
CYP1B1	1.44	0.0180	CYP1B1	NM_000104
DLC1	1.43	0.0012	DLC1	NM_006094
SI	1.43	0.0063	SI	NM_001041
CCNE2 variant 1	1.43	0.0506	CCNE2	NM_057749
LAMC2	1.42	0.0003	LAMC2	NM_005562
TIMP2	1.42	0.0018	TIMP2	NM_003255
CDC42BPA	1.42	0.0029	CDC42BPA	NM_003607
p21	1.41	0.0062	CDKN1A	NM_000389
HB-EGF	1.40	0.0105	HBEGF	NM_001945
TLN1	1.40	0.0260	TLN1	NM_006289
DUSP1	1.39	<.0001	DUSP1	NM_004417
ROCK1	1.39	0.0121	ROCK1	NM_005406
CTSB	1.39	0.0307	CTSB	NM_001908
ITGAV	1.38	0.0020	ITGAV	NM_002210
HSPG2	1.38	0.0215	HSPG2	NM_005529
GADD45B	1.37	0.0002	GADD45B	NM_015675
VCL	1.37	0.0201	VCL	NM_003373
SBA2	1.37	0.0250	WSB2	NM_018639
Maspin	1.36	<.0001	SERPINB5	NM_002639
CGB	1.36	0.0018	CGB	NM_000737
TIMP3	1.36	0.0024	TIMP3	NM_000362
VIM	1.36	0.0073	VIM	NM_003380
S100A1	1.36	0.0247	S100A1	NM_006271
INHBA	1.35	0.0008	INHBA	NM_002192
SIR2	1.35	0.0039	SIRT1	NM_012238
TMSB10	1.35	0.0469	TMSB10	NM_021103
CD68	1.34	0.0036	CD68	NM_001251
RBX1	1.34	0.0469	RBX1	NM_014248
INHBB	1.34	0.0514	INHBB	NM_002193
PKR2	1.34	0.0628	PKM2	NM_002654
FOS	1.33	0.0006	FOS	NM_005252
FYN	1.33	0.0036	FYN	NM_002037
LOXL2	1.33	0.0064	LOXL2	NM_002318
STC1	1.33	0.0101	STC1	NM_003155
DKK1	1.33	0.0208	DKK1	NM_012242
IGFBP5	1.32	0.0064	IGFBP5	NM_000599
EPAS1	1.32	0.0270	EPAS1	NM_001430
UNC5C	1.32	0.0641	UNC5C	NM_003728
FAP	1.31	0.0017	FAP	NM_004460
IGFBP3	1.31	0.0041	IGFBP3	NM_000598
SNAI2	1.31	0.0055	SNAI2	NM_003068
PRKCA	1.31	0.0065	PRKCA	NM_002737
FST	1.31	0.0399	FST	NM_006350
KCNH2 iso a/b	1.31	0.0950	KCNH2	NM_000238
CTHRC1	1.30	0.0017	CTHRC1	NM_138455
PDGFC	1.30	0.0034	PDGFC	NM_016205
EGR1	1.30	0.0048	EGR1	NM_001964
TAGLN	1.30	0.0058	TAGLN	NM_003186
SPARC	1.30	0.0104	SPARC	NM_003118
KLF6	1.30	0.0514	KLF6	NM_001300
GRIK1	1.30	0.0753	GRIK1	NM_000830
CYR61	1.29	0.0018	CYR61	NM_001554
SLPI	1.29	0.0026	SLPI	NM_003064
COL1A2	1.29	0.0076	COL1A2	NM_000089
MAPK14	1.29	0.0916	MAPK14	NM_139012
LAMA3	1.28	0.0020	LAMA3	NM_000227
THBS1	1.28	0.0053	THBS1	NM_003246
NRP2	1.28	0.0120	NRP2	NM_003872
LOX	1.27	0.0028	LOX	NM_002317
S100A4	1.27	0.0067	S100A4	NM_002961
CXCR4	1.27	0.0083	CXCR4	NM_003467

TABLE 1A-continued

Gene	Hazard Ratio	P Value	OfficialSymbol	Accession Number
CEBPB	1.27	0.0943	CEBPB	NM_005194
AKAP12	1.26	0.0044	AKAP12	NM_005100
ADAMTS12	1.26	0.0100	ADAMTS12	NM_030955
CRYAB	1.25	0.0038	CRYAB	NM_001885
Grb10	1.25	0.0108	GRB10	NM_005311
MCP1	1.25	0.0118	CCL2	NM_002982
COL1A1	1.25	0.0167	COL1A1	NM_000088
EFNB2	1.25	0.0241	EFNB2	NM_004093
ANXA1	1.25	0.0292	ANXA1	NM_000700
ANGPT2	1.25	0.0485	ANGPT2	NM_001147
EphB6	1.25	0.0825	EPHB6	NM_004445
HSPA1A	1.24	0.0018	HSPA1A	NM_005345
TGFB3	1.24	0.0081	TGFB3	NM_003239
PTGER3	1.24	0.0306	PTGER3	NM_000957
FXYD5	1.24	0.0367	FXYD5	NM_014164
CAPG	1.24	0.0604	CAPG	NM_001747
PDGFB	1.23	0.0157	PDGFB	NM_002608
ANTXR1	1.23	0.0164	ANTXR1	NM_032208
TGFBI	1.23	0.0191	TGFBI	NM_000358
CTGF	1.23	0.0233	CTGF	NM_001901
PDGFA	1.23	0.0274		NM_002607
P14ARF	1.23	0.0362		S78535
KLK10	1.22	0.0005	KLK10	NM_002776
ITGA5	1.22	0.0178	ITGA5	NM_002205
GBP2	1.22	0.0201	GBP2	NM_004120
SIAT4A	1.22	0.0231	ST3GAL1	NM_003033
GJB2	1.22	0.0271	GJB2	NM_004004
LAT	1.22	0.0306	LAT	NM_014387
CTSL	1.22	0.0331	CTSL	NM_001912
DAPK1	1.22	0.0384	DAPK1	NM_004938
SKP1A	1.22	0.0542	SKP1A	NM_006930
NDRG1	1.22	0.0712	NDRG1	NM_006096
ITGB5	1.22	0.0991	ITGB5	NM_002213
KLK6	1.21	0.0034	KLK6	NM_002774
SFRP2	1.21	0.0037	SFRP2	NM_003013
TMEPAI	1.21	0.0173	TMEPAI	NM_020182
ID4	1.21	0.0530	ID4	NM_001546
SFRP4	1.20	0.0077	SFRP4	NM_003014
HOXB7	1.20	0.0274	HOXB7	NM_004502
GJA1	1.20	0.0311	GJA1	NM_000165
CDH11	1.20	0.0662	CDH11	NM_001797
PAI1	1.19	0.0060	SERPINE1	NM_000602
S100P	1.19	0.0119	S100P	NM_005980
EGR3	1.19	0.0164	EGR3	NM_004430
EMP1	1.19	0.0460	EMP1	NM_001423
ABCC5	1.19	0.0536	ABCC5	NM_005688
FZD1	1.19	0.0701	FZD1	NM_003505
MAD	1.19	0.0811	MXD1	NM_002357
EFNA1	1.19	0.0920	EFNA1	NM_004428
OPN_osteopontin	1.18	0.0028	SPP1	NM_000582
ALDH1A1	1.18	0.0246	ALDH1A1	NM_000689
NR4A1	1.18	0.0277	NR4A1	NM_002135
SIAT7B	1.18	0.0301	ST6GALNAC2	NM_006456
p16-INK4	1.18	0.0439		L27211
TUBB	1.18	0.0761	TUBB2	NM_001069
IL6	1.18	0.0939	IL6	NM_000600
RAB32	1.18	0.0948	RAB32	NM_006834
TULP3	1.18	0.0953	TULP3	NM_003324
F3	1.17	0.0561	F3	NM_001993
PLK3	1.16	0.0792	PLK3	NM_004073
EPHA2	1.16	0.0962	EPHA2	NM_004431
SLC2A1	1.15	0.0745	SLC2A1	NM_006516
CXCL12	1.14	0.0911	CXCL12	NM_000609
S100A2	1.13	0.0287	S100A2	NM_005978
FABP4	1.13	0.0340	FABP4	NM_001442
STMY3	1.13	0.0517	MMP11	NM_005940
BCAS1	1.13	0.0939	BCAS1	NM_003657
REG4	1.11	0.0026	REG4	NM_032044
pS2	1.09	0.0605	TFF1	NM_003225
MUC2	1.06	0.0626	MUC2	NM_002457

Table 1B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using RFI as the metric for clinical outcome.

TABLE 1B

Gene	Hazard Ratio	P Value	OfficialSymbol	Accession Number
ORC1L	0.42	0.0728	ORC1L	NM_004153
HSPA8	0.62	0.0430	HSPA8	NM_006597
E2F1	0.64	0.0009	E2F1	NM_005225
RAD54L	0.65	0.0026	RAD54L	NM_003579
RPLPO	0.67	0.0150	RPLP0	NM_001002
BRCA1	0.68	0.0001	BRCA1	NM_007295
DHFR	0.69	0.0096	DHFR	NM_000791
SLC25A3	0.69	0.0110	SLC25A3	NM_213611
PPM1D	0.71	0.0033	PPM1D	NM_003620
SKP2	0.71	0.0098	SKP2	NM_005983
FASN	0.72	0.0071	FASN	NM_004104
HNRPD	0.72	0.0686	HNRPD	NM_031370
ENO1	0.73	0.0418	ENO1	NM_001428
RPS13	0.75	0.0786	RPS13	NM_001017
DDB1	0.75	0.0804	DDB1	NM_001923
C20 orf1	0.76	0.0122	TPX2	NM_012112
KIF22	0.76	0.0137	KIF22	NM_007317
Chk1	0.76	0.0174	CHEK1	NM_001274
TCF-1	0.77	0.0021	TCF1	NM_000545
ST14	0.77	0.0446	ST14	NM_021978
RRM1	0.77	0.0740	RRM1	NM_001033
BRCA2	0.77	0.0800	BRCA2	NM_000059
LMNB1	0.78	0.0513	LMNB1	NM_005573
CMYC	0.79	0.0086	MYC	NM_002467
CDC20	0.79	0.0290	CDC20	NM_001255
CSEL1	0.79	0.0344	CSE1L	NM_001316
Bax	0.79	0.0662	BAX	NM_004324
NME1	0.79	0.0742	NME1	NM_000269
c-myb (MYB official)	0.80	0.0077	MYB	NM_005375
CDCA7 v2	0.80	0.0159	CDCA7	NM_145810
EFP	0.80	0.0405	TRIM25	NM_005082
UBE2M	0.80	0.0437	UBE2M	NM_003969
RRM2	0.81	0.0168	RRM2	NM_001034
ABCC6	0.81	0.0373	ABCC6	NM_001171
SURV	0.81	0.0584	BIRC5	NM_001168
CKS2	0.81	0.0753	CKS2	NM_001827
RAF1	0.81	0.0899	RAF1	NM_002880
EPHB2	0.82	0.0190	EPHB2	NM_004442
NOTCH1	0.82	0.0232	NOTCH1	NM_017617
UMPS	0.82	0.0456	UMPS	NM_000373
CCNE2	0.82	0.0544	CCNE2	NM_057749
PI3KC2A	0.82	0.0916	PIK3C2A	NM_002645
CD80	0.82	0.0954	CD80	NM_005191
AREG	0.83	0.0014	AREG	NM_001657
EREG	0.83	0.0062	EREG	NM_001432
MYBL2	0.83	0.0259	MYBL2	NM_002466
ABCB1	0.83	0.0322	ABCB1	NM_000927
HRAS	0.83	0.0760	HRAS	NM_005343
SLC7A5	0.84	0.0585	SLC7A5	NM_003486
MAD2L1	0.84	0.0590	MAD2L1	NM_002358
Ki-67	0.85	0.0620	MKI67	NM_002417
MCM2	0.85	0.0700	MCM2	NM_004526
ING5	0.85	0.0947	ING5	NM_032329
Cdx2	0.88	0.0476	CDX2	NM_001265
PTPRO	0.89	0.0642	PTPRO	NM_030667
cripto (TDGF1 official)	0.90	0.0803	TDGF1	NM_003212

Table 2A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using OS as the metric for clinical outcome.

TABLE 2A

Gene	Hazard Ratio	P Value	OfficialSymbol	Accession Number
RARB	1.75	0.0820	RARB	NM_016152
RhoC	1.70	0.0001	RHOC	NM_175744
ANXA2	1.64	0.0002	ANXA2	NM_004039
CYP3A4	1.58	0.0064	CYP3A4	NM_017460
p21	1.54	<.0001	CDKN1A	NM_000389
ITGB1	1.54	0.0058	ITGB1	NM_002211
UBC	1.50	0.0003	UBC	NM_021009
TNF	1.46	0.0859	TNF	NM_000594
VEGFC	1.44	0.0049	VEGFC	NM_005429
HMLH	1.44	0.0435	MLH1	NM_000249
RhoB	1.37	0.0015	RHOB	NM_004040
TGFBR1	1.37	0.0127	TGFBR1	NM_004612
SPINT2	1.37	0.0235	SPINT2	NM_021102
PFN1	1.37	0.0842	PFN1	NM_005022
HSPG2	1.36	0.0115	HSPG2	NM_005529
TIMP1	1.35	0.0008	TIMP1	NM_003254
INHBB	1.35	0.0190	INHBB	NM_002193
VCL	1.34	0.0099	VCL	NM_003373
KCNH2 iso a/b	1.33	0.0362	KCNH2	NM_000238
LAMC2	1.32	0.0005	LAMC2	NM_005562
FXYD5	1.31	0.0021	FXYD5	NM_014164
HLA-G	1.31	0.0458	HLA-G	NM_002127
GADD45B	1.30	0.0002	GADD45B	NM_015675
CDC42	1.30	0.0120	CDC42	NM_001791
LAMB3	1.30	0.0163	LAMB3	NM_000228
DKK1	1.30	0.0209	DKK1	NM_012242
UNC5C	1.30	0.0452	UNC5C	NM_003728
UBL1	1.29	0.0171	SUMO1	NM_003352
HB-EGF	1.29	0.0262	HBEGF	NM_001945
KRAS2	1.29	0.0726	KRAS	NM_004985
ID3	1.28	0.0023	ID3	NM_002167
LOXL2	1.28	0.0039	LOXL2	NM_002318
EphB6	1.28	0.0322	EPHB6	NM_004445
DUSP1	1.27	0.0003	DUSP1	NM_004417
BGN	1.27	0.0040	BGN	NM_001711
CALD1	1.27	0.0119	CALD1	NM_004342
CDC42BPA	1.27	0.0151	CDC42BPA	NM_003607
SBA2	1.27	0.0373	WSB2	NM_018639
INHBA	1.26	0.0018	INHBA	NM_002192
NRP1	1.26	0.0113	NRP1	NM_003873
TIMP2	1.26	0.0123	TIMP2	NM_003255
KLF6	1.26	0.0444	KLF6	NM_001300
KLK10	1.25	<.0001	KLK10	NM_002776
TIMP3	1.25	0.0083	TIMP3	NM_000362
CAPG	1.25	0.0170	CAPG	NM_001747
IGFBP7	1.25	0.0249	IGFBP7	NM_001553
S100A1	1.25	0.0529	S100A1	NM_006271
SHC1	1.25	0.0605	SHC1	NM_003029
CTSB	1.25	0.0766	CTSB	NM_001908
ANXA5	1.25	0.0787	ANXA5	NM_001154
PKR2	1.25	0.0800	PKM2	NM_002654
HSPA1A	1.24	0.0003	HSPA1A	NM_005345
CGB	1.24	0.0148	CGB	NM_000737
DLC1	1.24	0.0231	DLC1	NM_006094
TMSB10	1.24	0.0890	TMSB10	NM_021103
LAMA3	1.23	0.0017	LAMA3	NM_000227
FOS	1.23	0.0028	FOS	NM_005252
SNAI2	1.23	0.0123	SNAI2	NM_003068
SPARC	1.23	0.0134	SPARC	NM_003118
SIR2	1.23	0.0173	SIRT1	NM_012238
KRT19	1.23	0.0217	KRT19	NM_002276
CTSD	1.23	0.0395	CTSD	NM_001909
EPAS1	1.23	0.0409	EPAS1	NM_001430
GAGE4	1.23	0.0468	GAGE4	NM_001474
BMP4	1.22	0.0024	BMP4	NM_001202
PLK3	1.22	0.0056	PLK3	NM_004073
Grb10	1.22	0.0059	GRB10	NM_005311
FYN	1.22	0.0120	FYN	NM_002037
STC1	1.22	0.0409	STC1	NM_003155
G-Catenin	1.22	0.0661	JUP	NM_002230
HK1	1.22	0.0872	HK1	NM_000188
MADH4	1.22	0.0956	SMAD4	NM_005359
KLK6	1.21	0.0011	KLK6	NM_002774
CTHRC1	1.21	0.0065	CTHRC1	NM_138455
LAT	1.21	0.0146	LAT	NM_014387
IGFBP3	1.21	0.0149	IGFBP3	NM_000598
AKT3	1.21	0.0212	AKT3	NM_005465
HSPA1B	1.21	0.0262	HSPA1B	NM_005346
THY1	1.21	0.0278	THY1	NM_006288
ANXA1	1.21	0.0322	ANXA1	NM_000700
LOX	1.20	0.0067	LOX	NM_002317
CD68	1.20	0.0223	CD68	NM_001251
EFNB2	1.20	0.0268	EFNB2	NM_004093
DYRK1B	1.20	0.0473	DYRK1B	NM_004714
PTK2	1.20	0.0889	PTK2	NM_005607
THBS1	1.19	0.0203	THBS1	NM_003246
TAGLN	1.19	0.0263	TAGLN	NM_003186
TULP3	1.19	0.0334	TULP3	NM_003324
SR-A1	1.19	0.0387	SR-A1	NM_021228
APC	1.19	0.0433	APC	NM_000038
ERK1	1.19	0.0488		Z11696
VIM	1.19	0.0661	VIM	NM_003380
CREBBP	1.19	0.0802	CREBBP	NM_004380
ANGPT2	1.19	0.0860	ANGPT2	NM_001147
Maspin	1.18	0.0029	SERPINB5	NM_002639
PDGFB	1.18	0.0252	PDGFB	NM_002608
S100A4	1.18	0.0270	S100A4	NM_002961
EGR1	1.18	0.0334	EGR1	NM_001964
IGFBP5	1.18	0.0526	IGFBP5	NM_000599
NOTCH2	1.18	0.0527	NOTCH2	NM_024408
PAI1	1.17	0.0036	SERPINE1	NM_000602
NR4A1	1.17	0.0110	NR4A1	NM_002135
BCAS1	1.17	0.0137	BCAS1	NM_003657
BRK	1.17	0.0137	PTK6	NM_005975
AKAP12	1.17	0.0195	AKAP12	NM_005100
EMP1	1.17	0.0291	EMP1	NM_001423
SIAT4A	1.17	0.0304	ST3GAL1	NM_003033
MRP3	1.17	0.0334	ABCC3	NM_003786
COL1A1	1.17	0.0399	COL1A1	NM_000088
Upa	1.17	0.0588	PLAU	NM_002658
UNC5B	1.17	0.0986	UNC5B	NM_170744
PDGFC	1.16	0.0355	PDGFC	NM_016205
MCP1	1.16	0.0449	CCL2	NM_002982
CTGF	1.16	0.0576	CTGF	NM_001901
COL1A2	1.16	0.0612	COL1A2	NM_000089
RAB32	1.16	0.0645	RAB32	NM_006834
SIN3A	1.16	0.0787	SIN3A	NM_015477
SKP1A	1.16	0.0837	SKP1A	NM_006930
EFNA1	1.16	0.0957	EFNA1	NM_004428
S100A2	1.15	0.0040	S100A2	NM_005978
MMP7	1.15	0.0374	MMP7	NM_002423
HOXB7	1.15	0.0405	HOXB7	NM_004502
FAP	1.15	0.0455	FAP	NM_004460
ANTXR1	1.15	0.0482	ANTXR1	NM_032208
TGFBI	1.15	0.0553	TGFBI	NM_000358
TMEPAI	1.14	0.0435	TMEPAI	NM_020182
CYR61	1.14	0.0490	CYR61	NM_001554
SLPI	1.14	0.0724	SLPI	NM_003064
TP53I3	1.14	0.0831	TP53I3	NM_004881
PDGFA	1.14	0.0845		NM_002607
SFRP2	1.13	0.0255	SFRP2	NM_003013
S100A8	1.13	0.0693	S100A8	NM_002964
F3	1.13	0.0708	F3	NM_001993
Bcl2	1.13	0.0962	BCL2	NM_000633
OPN_osteopontin	1.12	0.0097	SPP1	NM_000582
FZD6	1.12	0.0692	FZD6	NM_003506
OSM	1.11	0.0744	OSM	NM_020530
EGLN3	1.11	0.0884	EGLN3	NM_022073
SIAT7B	1.11	0.0938	ST6GALNAC2	NM_006456
FABP4	1.10	0.0454	FABP4	NM_001442
EFNA3	1.10	0.0958	EFNA3	NM_004952
MMP2	1.10	0.0969	MMP2	NM_004530
GSTT1	1.09	0.0737	GSTT1	NM_000853
REG4	1.07	0.0286	REG4	NM_032044

Table 2B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using OS as the metric for clinical outcome.

TABLE 2B

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
HSPA8	0.62	0.0145	HSPA8	NM_006597
SKP2	0.70	0.0010	SKP2	NM_005983
DHFR	0.74	0.0085	DHFR	NM_000791
PRDX4	0.74	0.0197	PRDX4	NM_006406
RRM1	0.75	0.0162	RRM1	NM_001033
SLC25A3	0.75	0.0342	SLC25A3	NM_213611
RPLPO	0.75	0.0416	RPLP0	NM_001002
E2F1	0.78	0.0190	E2F1	NM_005225
SURV	0.79	0.0086	BIRC5	NM_001168
c-myb (MYB official)	0.80	0.0020	MYB	NM_005375
BRCA1	0.80	0.0077	BRCA1	NM_007295
Chk1	0.80	0.0186	CHEK1	NM_001274
ST14	0.80	0.0407	ST14	NM_021978
TCF-1	0.81	0.0045	TCF1	NM_000545
CCNE2	0.81	0.0112	CCNE2	NM_057749
PPM1D	0.81	0.0194	PPM1D	NM_003620
CDC20	0.81	0.0213	CDC20	NM_001255
EI24	0.81	0.0585	EI24	NM_004879
C20 orf1	0.82	0.0348	TPX2	NM_012112
DUT	0.83	0.0396	DUT	NM_001948
CD44E	0.83	0.0439		X55150
KIF22	0.83	0.0506	KIF22	NM_007317
PPID	0.83	0.0615	PPID	NM_005038
UBE2M	0.83	0.0805	UBE2M	NM_003969
LMNB1	0.83	0.0868	LMNB1	NM_005573
MCM2	0.84	0.0207	MCM2	NM_004526
CDC6	0.84	0.0218	CDC6	NM_001254
MRPL40	0.84	0.0769	MRPL40	NM_003776
EPHB2	0.85	0.0253	EPHB2	NM_004442
CMYC	0.85	0.0371	MYC	NM_002467
AURKB	0.85	0.0375	AURKB	NM_004217
CDCA7 v2	0.85	0.0421	CDCA7	NM_145810
ABCB1	0.86	0.0390	ABCB1	NM_000927
SMARCA3	0.86	0.0601	SMARCA3	NM_003071
Cdx2	0.88	0.0166	CDX2	NM_001265
PPARG	0.88	0.0645	PPARG	NM_005037
MYBL2	0.88	0.0647	MYBL2	NM_002466
EREG	0.89	0.0411	EREG	NM_001432
AREG	0.90	0.0235	AREG	NM_001657

Table 3A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DFS as the metric for clinical outcome.

TABLE 3A

Gene	Hazard Ratio	P Value	OfficialSymbol	Accession Number
ANXA2	1.74	<.0001	ANXA2	NM_004039
CYP3A4	1.69	0.0020	CYP3A4	NM_017460
RhoC	1.53	0.0009	RHOC	NM_175744
TJP1	1.45	0.0787	TJP1	NM_003257
UBC	1.43	0.0007	UBC	NM_021009
p21	1.42	0.0004	CDKN1A	NM_000389
HB-EGF	1.39	0.0032	HBEGF	NM_001945
SPINT2	1.37	0.0154	SPINT2	NM_021102
HMLH	1.36	0.0711	MLH1	NM_000249
VEGFC	1.35	0.0157	VEGFC	NM_005429
PKR2	1.34	0.0187	PKM2	NM_002654
LAMC2	1.33	0.0002	LAMC2	NM_005562
ITGB1	1.33	0.0499	ITGB1	NM_002211
TIMP1	1.32	0.0007	TIMP1	NM_003254
VCL	1.31	0.0114	VCL	NM_003373
INHBB	1.31	0.0302	INHBB	NM_002193
GADD45B	1.30	<.0001	GADD45B	NM_015675
RhoB	1.30	0.0053	RHOB	NM_004040
DUSP1	1.28	<.0001	DUSP1	NM_004417
HK1	1.28	0.0297	HK1	NM_000188
GRIK1	1.28	0.0364	GRIK1	NM_000830
FOS	1.27	0.0002	FOS	NM_005252
CGB	1.27	0.0126	CGB	NM_000737
KLF6	1.27	0.0288	KLF6	NM_001300
ANXA5	1.27	0.0504	ANXA5	NM_001154
KRAS2	1.27	0.0724	KRAS	NM_004985
INHBA	1.26	0.0009	INHBA	NM_002192
DLC1	1.26	0.0096	DLC1	NM_006094
IGFBP7	1.26	0.0116	IGFBP7	NM_001553
BGN	1.25	0.0039	BGN	NM_001711
LOXL2	1.25	0.0076	LOXL2	NM_002318
STC1	1.25	0.0135	STC1	NM_003155
CTSD	1.25	0.0208	CTSD	NM_001909
HSPG2	1.25	0.0485	HSPG2	NM_005529
KCNH2 iso a/b	1.25	0.0832	KCNH2	NM_000238
TIMP3	1.24	0.0057	TIMP3	NM_000362
FXYD5	1.24	0.0070	FXYD5	NM_014164
A-Catenin	1.24	0.0447	CTNNA1	NM_001903
LOX	1.23	0.0013	LOX	NM_002317
EGR1	1.23	0.0037	EGR1	NM_001964
CAPG	1.23	0.0191	CAPG	NM_001747
LAMB3	1.23	0.0377	LAMB3	NM_000228
GAGE4	1.23	0.0402	GAGE4	NM_001474
SHC1	1.23	0.0640	SHC1	NM_003029
MVP	1.23	0.0726	MVP	NM_017458
VEGF	1.22	0.0250	VEGF	NM_003376
UNC5B	1.22	0.0256	UNC5B	NM_170744
CDC42BPA	1.22	0.0297	CDC42BPA	NM_003607
SBA2	1.22	0.0614	WSB2	NM_018639
DKK1	1.22	0.0689	DKK1	NM_012242
EphB6	1.22	0.0763	EPHB6	NM_004445
IGFBP3	1.21	0.0078	IGFBP3	NM_000598
HSPA1B	1.21	0.0167	HSPA1B	NM_005346
CALD1	1.21	0.0277	CALD1	NM_004342
TIMP2	1.21	0.0309	TIMP2	NM_003255
NR4A1	1.20	0.0023	NR4A1	NM_002135
LAMA3	1.20	0.0028	LAMA3	NM_000227
SIAT4A	1.20	0.0082	ST3GAL1	NM_003033
PDGFB	1.20	0.0084	PDGFB	NM_002608
EMP1	1.20	0.0107	EMP1	NM_001423
THBS1	1.20	0.0126	THBS1	NM_003246
CD68	1.20	0.0143	CD68	NM_001251
FYN	1.20	0.0151	FYN	NM_002037
TULP3	1.20	0.0213	TULP3	NM_003324
EFNA1	1.20	0.0254	EFNA1	NM_004428
SIR2	1.20	0.0255	SIRT1	NM_012238
G-Catenin	1.20	0.0689	JUP	NM_002230
S100A1	1.20	0.0998	S100A1	NM_006271
Maspin	1.19	0.0013	SERPINB5	NM_002639
HSPA1A	1.19	0.0013	HSPA1A	NM_005345
SPARC	1.19	0.0359	SPARC	NM_003118
PTHR1	1.19	0.0801	PTHR1	NM_000316
SNAI2	1.18	0.0353	SNAI2	NM_003068
KRT19	1.18	0.0419	KRT19	NM_002276
ERK1	1.18	0.0459		Z11696
KLK10	1.17	0.0007	KLK10	NM_002776
BMP4	1.17	0.0121	BMP4	NM_001202
CYR61	1.17	0.0127	CYR61	NM_001554
Grb10	1.17	0.0216	GRB10	NM_005311
PLK3	1.17	0.0242	PLK3	NM_004073
EFNB2	1.17	0.0403	EFNB2	NM_004093
P14ARF	1.17	0.0439		S78535
ID3	1.17	0.0446	ID3	NM_002167
IGFBP5	1.17	0.0503	IGFBP5	NM_000599
THY1	1.17	0.0574	THY1	NM_006288
VIM	1.17	0.0858	VIM	NM_003380
EPAS1	1.17	0.0897	EPAS1	NM_001430
PAI1	1.16	0.0039	SERPINE1	NM_000602
F3	1.16	0.0172	F3	NM_001993
CTHRC1	1.16	0.0181	CTHRC1	NM_138455
ANTXR1	1.16	0.0237	ANTXR1	NM_032208
FAP	1.16	0.0289	FAP	NM_004460
ADAMTS12	1.16	0.0350	ADAMTS12	NM_030955
CTGF	1.16	0.0424	CTGF	NM_001901
PTGER3	1.16	0.0569	PTGER3	NM_000957
ANXA1	1.16	0.0699	ANXA1	NM_000700

TABLE 3A-continued

Gene	Hazard Ratio	P Value	OfficialSymbol	Accession Number
NRP1	1.16	0.0797	NRP1	NM_003873
NDRG1	1.16	0.0856	NDRG1	NM_006096
KLK6	1.15	0.0092	KLK6	NM_002774
EGR3	1.15	0.0153	EGR3	NM_004430
HOXB7	1.15	0.0345	HOXB7	NM_004502
PDGFC	1.15	0.0363	PDGFC	NM_016205
Herstatin	1.15	0.0403		AF177761
MCP1	1.15	0.0409	CCL2	NM_002982
TGFBI	1.15	0.0437	TGFBI	NM_000358
TP53I3	1.15	0.0438	TP53I3	NM_004881
SLPI	1.15	0.0457	SLPI	NM_003064
PLAUR	1.15	0.0471	PLAUR	NM_002659
GJB2	1.15	0.0610	GJB2	NM_004004
COL1A1	1.15	0.0647	COL1A1	NM_000088
IL6	1.15	0.0790	IL6	NM_000600
APC	1.15	0.0821	APC	NM_000038
S100A2	1.14	0.0048	S100A2	NM_005978
TMEPAI	1.14	0.0300	TMEPAI	NM_020182
PDGFA	1.14	0.0644		NM_002607
S100A4	1.14	0.0680	S100A4	NM_002961
TAGLN	1.14	0.0820	TAGLN	NM_003186
Upa	1.14	0.0823	PLAU	NM_002658
COL1A2	1.14	0.0856	COL1A2	NM_000089
OSM	1.13	0.0299	OSM	NM_020530
BRK	1.13	0.0479	PTK6	NM_005975
SEMA3B	1.13	0.0525	SEMA3B	NM_004636
OPN_osteopontin	1.12	0.0084	SPP1	NM_000582
S100P	1.12	0.0283	S100P	NM_005980
SFRP2	1.12	0.0291	SFRP2	NM_003013
EGLN3	1.12	0.0465	EGLN3	NM_022073
SIAT7B	1.12	0.0570	ST6GALNAC2	NM_006456
MMP7	1.12	0.0743	MMP7	NM_002423
FABP4	1.11	0.0195	FABP4	NM_001442
AKAP12	1.11	0.0899	AKAP12	NM_005100
EFNA3	1.10	0.0684	EFNA3	NM_004952
SFRP4	1.10	0.0684	SFRP4	NM_003014
CRYAB	1.10	0.0987	CRYAB	NM_001885
GSTT1	1.09	0.0457	GSTT1	NM_000853
REG4	1.08	0.0074	REG4	NM_032044
pS2	1.08	0.0302	TFF1	NM_003225
MUC5B	1.08	0.0401	MUC5B	XM_039877
IGFBP2	1.08	0.0873	IGFBP2	NM_000597

Table 3B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DFS as the metric for clinical outcome.

TABLE 3B

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
HSPA8	0.70	0.0487	HSPA8	NM_006597
SLC25A3	0.71	0.0084	SLC25A3	NM_213611
E2F1	0.73	0.0019	E2F1	NM_005225
SKP2	0.73	0.0038	SKP2	NM_005983
PPM1D	0.75	0.0008	PPM1D	NM_003620
RRM1	0.76	0.0161	RRM1	NM_001033
RPLPO	0.76	0.0388	RPLP0	NM_001002
NPM1	0.78	0.0223	NPM1	NM_002520
DDB1	0.78	0.0673	DDB1	NM_001923
PRDX4	0.79	0.0526	PRDX4	NM_006406
BRCA1	0.80	0.0051	BRCA1	NM_007295
Chk1	0.80	0.0114	CHEK1	NM_001274
SURV	0.81	0.0155	BIRC5	NM_001168
C20 orf1	0.81	0.0195	TPX2	NM_012112
EI24	0.81	0.0382	EI24	NM_004879
RAD54L	0.81	0.0501	RAD54L	NM_003579
DHFR	0.81	0.0530	DHFR	NM_000791
c-myb (MYB official)	0.82	0.0029	MYB	NM_005375
CCNE2	0.82	0.0109	CCNE2	NM_057749
KIF22	0.82	0.0235	KIF22	NM_007317
HMGB1	0.82	0.0849	HMGB1	NM_002128
LMNB1	0.83	0.0665	LMNB1	NM_005573
CDCA7 v2	0.84	0.0224	CDCA7	NM_145810
CDC20	0.84	0.0461	CDC20	NM_001255
FASN	0.84	0.0797	FASN	NM_004104
ABCB1	0.85	0.0157	ABCB1	NM_000927
MCM2	0.85	0.0183	MCM2	NM_004526
DUT	0.85	0.0469	DUT	NM_001948
KIF2C	0.85	0.0786	KIF2C	NM_006845
MCM6	0.85	0.0791	MCM6	NM_005915
EIF4E	0.85	0.0863	EIF4E	NM_001968
EPHB2	0.86	0.0271	EPHB2	NM_004442
RCC1	0.86	0.0444	RCC1	NM_001269
EFP	0.86	0.0760	TRIM25	NM_005082
AREG	0.87	0.0029	AREG	NM_001657
CMYC	0.87	0.0483	MYC	NM_002467
GCLC	0.87	0.0824	GCLC	NM_001498
TCF-1	0.88	0.0520	TCF1	NM_000545
MYBL2	0.88	0.0527	MYBL2	NM_002466
EREG	0.89	0.0237	EREG	NM_001432
Cdx2	0.90	0.0353	CDX2	NM_001265
PTPRO	0.92	0.0896	PTPRO	NM_030667
cripto (TDGF1 official)	0.92	0.0913	TDGF1	NM_003212
HLA-DRB1	0.93	0.0536	HLA-DRB1	NM_002124

Table 4A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DRFI as the metric for clinical outcome.

TABLE 4A

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
ALDOA	3.37	0.0106	ALDOA	NM_000034
DCK	2.74	0.0130	DCK	NM_000788
ITGB1	2.50	<.0001	ITGB1	NM_002211
COX2	2.15	0.0128	PTGS2	NM_000963
TJP1	2.12	0.0072	TJP1	NM_003257
STAT3	1.98	0.0062	STAT3	NM_003150
HMLH	1.93	0.0087	MLH1	NM_000249
CYP3A4	1.90	0.0092	CYP3A4	NM_017460
RhoC	1.89	0.0033	RHOC	NM_175744
ANXA2	1.87	0.0025	ANXA2	NM_004039
TIMP1	1.83	<.0001	TIMP1	NM_003254
WWOX	1.81	0.0288	WWOX	NM_016373
ANXA5	1.80	0.0029	ANXA5	NM_001154
FUS	1.79	0.0179	FUS	NM_004960
PADI4	1.78	0.0168	PADI4	NM_012387
RBX1	1.71	0.0082	RBX1	NM_014248
CRIP2	1.71	0.0343	CRIP2	NM_001312
HB-EGF	1.69	0.0013	HBEGF	NM_001945
KCNH2 iso a/b	1.69	0.0070	KCNH2	NM_000238
SBA2	1.68	0.0066	WSB2	NM_018639
RhoB	1.67	0.0010	RHOB	NM_004040
VIM	1.66	0.0010	VIM	NM_003380
LILRB3	1.66	0.0227	LILRB3	NM_006864
UBC	1.64	0.0051	UBC	NM_021009
p21	1.63	0.0032	CDKN1A	NM_000389
CCNE2 variant 1	1.62	0.0363	CCNE2	NM_057749
RAB6C	1.61	0.0107	RAB6C	NM_032144
MSH3	1.61	0.0213	MSH3	NM_002439
AKT3	1.59	0.0003	AKT3	NM_005465
PI3K	1.58	0.0552	PIK3C2B	NM_002646
RAP1GDS1	1.57	0.0154	RAP1GDS1	NM_021159
CTSB	1.57	0.0250	CTSB	NM_001908

TABLE 4A-continued

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
PRDX6	1.57	0.0770	PRDX6	NM_004905
NRP2	1.56	0.0005	NRP2	NM_003872
DLC1	1.56	0.0026	DLC1	NM_006094
BGN	1.55	0.0006	BGN	NM_001711
SIR2	1.55	0.0016	SIRT1	NM_012238
CALD1	1.53	0.0046	CALD1	NM_004342
YWHAH	1.53	0.0429	YWHAH	NM_003405
CDC42	1.52	0.0207	CDC42	NM_001791
ITGA5	1.51	0.0004	ITGA5	NM_002205
KLF6	1.51	0.0197	KLF6	NM_001300
TLN1	1.51	0.0414	TLN1	NM_006289
LAMC2	1.49	0.0017	LAMC2	NM_005562
STC1	1.49	0.0040	STC1	NM_003155
CDC42BPA	1.49	0.0109	CDC42BPA	NM_003607
RBM5	1.49	0.0184	RBM5	NM_005778
INHBB	1.49	0.0310	INHBB	NM_002193
TGFBR1	1.49	0.0502	TGFBR1	NM_004612
ADAM10	1.49	0.0819	ADAM10	NM_001110
CEBPB	1.48	0.0399	CEBPB	NM_005194
AKT1	1.48	0.0846	AKT1	NM_005163
FYN	1.47	0.0036	FYN	NM_002037
ARG	1.47	0.0067	ABL2	NM_005158
HIF1A	1.47	0.0221	HIF1A	NM_001530
S100A1	1.47	0.0293	S100A1	NM_006271
KRAS2	1.47	0.0958	KRAS	NM_004985
CTHRC1	1.46	0.0008	CTHRC1	NM_138455
IGFBP7	1.46	0.0173	IGFBP7	NM_001553
ROCK1	1.46	0.0326	ROCK1	NM_005406
VEGFC	1.46	0.0516	VEGFC	NM_005429
EPAS1	1.45	0.0316	EPAS1	NM_001430
DUSP1	1.44	0.0008	DUSP1	NM_004417
FST	1.44	0.0340	FST	NM_006350
GADD45B	1.43	0.0013	GADD45B	NM_015675
FLT4	1.43	0.0663	FLT4	NM_002020
PTEN	1.43	0.0760	PTEN	NM_000314
FAP	1.42	0.0017	FAP	NM_004460
PDGFC	1.42	0.0033	PDGFC	NM_016205
LOXL2	1.42	0.0115	LOXL2	NM_002318
Pak1	1.42	0.0846	PAK1	NM_002576
Grb10	1.41	0.0020	GRB10	NM_005311
INHBA	1.41	0.0036	INHBA	NM_002192
GJA1	1.41	0.0039	GJA1	NM_000165
CTGF	1.41	0.0053	CTGF	NM_001901
COL1A2	1.41	0.0057	COL1A2	NM_000089
PTK2	1.40	0.0496	PTK2	NM_005607
THBS1	1.39	0.0059	THBS1	NM_003246
RANBP9	1.39	0.0333	RANBP9	NM_005493
RANBP2	1.39	0.0988	RANBP2	NM_006267
ITGAV	1.38	0.0210	ITGAV	NM_002210
TIMP2	1.38	0.0285	TIMP2	NM_003255
PTHR1	1.38	0.0297	PTHR1	NM_000316
GADD45	1.38	0.0340	GADD45A	NM_001924
c-abl	1.38	0.0526	ABL1	NM_005157
EGR1	1.37	0.0097	EGR1	NM_001964
NCAM1	1.37	0.0657	NCAM1	NM_000615
VCL	1.37	0.0845	VCL	NM_003373
LOX	1.36	0.0026	LOX	NM_002317
SNAI2	1.36	0.0178	SNAI2	NM_003068
SPARC	1.36	0.0198	SPARC	NM_003118
CDH11	1.36	0.0233	CDH11	NM_001797
NFKBp50	1.36	0.0767	NFKB1	NM_003998
CYR61	1.35	0.0065	CYR61	NM_001554
S100A4	1.35	0.0104	S100A4	NM_002961
TAGLN	1.35	0.0168	TAGLN	NM_003186
PCAF	1.34	0.0327	PCAF	NM_003884
NOTCH2	1.34	0.0390	NOTCH2	NM_024408
LRP5	1.34	0.0722	LRP5	NM_002335
SI	1.34	0.0787	SI	NM_001041
GBP2	1.33	0.0139	GBP2	NM_004120
Bcl2	1.33	0.0143	BCL2	NM_000633
MCP1	1.33	0.0159	CCL2	NM_002982
EPHA2	1.33	0.0184	EPHA2	NM_004431
PRKCA	1.33	0.0329	PRKCA	NM_002737
TIMP3	1.33	0.0337	TIMP3	NM_000362
ANGPT2	1.33	0.0476	ANGPT2	NM_001147
CTSD	1.33	0.0766	CTSD	NM_001909
SEMA3F	1.33	0.0931	SEMA3F	NM_004186
BCAS1	1.32	0.0044	BCAS1	NM_003657
ANXA1	1.32	0.0458	ANXA1	NM_000700
KRT19	1.32	0.0535	KRT19	NM_002276
PTPRJ	1.32	0.0618	PTPRJ	NM_002843
CAPG	1.32	0.0641	CAPG	NM_001747
FOS	1.31	0.0129	FOS	NM_005252
COL1A1	1.31	0.0236	COL1A1	NM_000088
CXCR4	1.31	0.0251	CXCR4	NM_003467
TUBB	1.31	0.0354	TUBB2	NM_001069
PIM1	1.31	0.0373	PIM1	NM_002648
IGFBP5	1.31	0.0477	IGFBP5	NM_000599
AP-1 (JUN official)	1.31	0.0519	JUN	NM_002228
GCNT1	1.31	0.0534	GCNT1	NM_001490
MAX	1.31	0.0650	MAX	NM_002382
PAI1	1.30	0.0017	SERPINE1	NM_000602
SLPI	1.30	0.0176	SLPI	NM_003064
IGFBP3	1.30	0.0320	IGFBP3	NM_000598
DAPK1	1.30	0.0402	DAPK1	NM_004938
ID3	1.30	0.0442	ID3	NM_002167
EFNA1	1.30	0.0623	EFNA1	NM_004428
AKAP12	1.29	0.0162	AKAP12	NM_005100
PDGFB	1.29	0.0242	PDGFB	NM_002608
CD68	1.29	0.0524	CD68	NM_001251
FGFR1	1.29	0.0709	FGFR1	NM_023109
GSK3B	1.29	0.0765	GSK3B	NM_002093
CXCL12	1.28	0.0129	CXCL12	NM_000609
DPYD	1.28	0.0186	DPYD	NM_000110
LAMA3	1.28	0.0193	LAMA3	NM_000227
MRP3	1.28	0.0384	ABCC3	NM_003786
ABCC5	1.28	0.0402	ABCC5	NM_005688
PDGFA	1.28	0.0482		NM_002607
XPA	1.28	0.0740	XPA	NM_000380
NDRG1	1.28	0.0786	NDRG1	NM_006096
FES	1.27	0.0458	FES	NM_002005
CTSL	1.27	0.0485	CTSL	NM_001912
IL6	1.27	0.0606	IL6	NM_000600
SFRP2	1.26	0.0085	SFRP2	NM_003013
Maspin	1.26	0.0096	SERPINB5	NM_002639
TGFBI	1.26	0.0470	TGFBI	NM_000358
NOS3	1.26	0.0978	NOS3	NM_000603
HSPA1A	1.25	0.0161	HSPA1A	NM_005345
S100A8	1.25	0.0180	S100A8	NM_002964
HOXB7	1.25	0.0396	HOXB7	NM_004502
P14ARF	1.25	0.0697		S78535
WISP1	1.25	0.0712	WISP1	NM_003882
ID4	1.25	0.0883	ID4	NM_001546
SFRP4	1.24	0.0200	SFRP4	NM_003014
FZD6	1.24	0.0220	FZD6	NM_003506
EGR3	1.24	0.0237	EGR3	NM_004430
ALDH1A1	1.24	0.0258	ALDH1A1	NM_000689
CRYAB	1.23	0.0394	CRYAB	NM_001885
TGFB3	1.23	0.0541	TGFB3	NM_003239
ANTXR1	1.23	0.0661	ANTXR1	NM_032208
KLK6	1.22	0.0211	KLK6	NM_002774
ILT-2	1.22	0.0676	LILRB1	NM_006669
EMP1	1.22	0.0871	EMP1	NM_001423
PLAUR	1.22	0.0943	PLAUR	NM_002659
S100A2	1.20	0.0100	S100A2	NM_005978
MMP7	1.19	0.0810	MMP7	NM_002423
OPN_osteopontin	1.17	0.0231	SPP1	NM_000582
FABP4	1.17	0.0325	FABP4	NM_001442
KLK10	1.17	0.0452	KLK10	NM_002776
PS2	1.16	0.0140	TFF1	NM_003225
STMY3	1.15	0.0850	MMP11	NM_005940
REG4	1.14	0.0042	REG4	NM_032044
MUC2	1.09	0.0370	MUC2	NM_002457

Table 4B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DRFI as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	OfficialSymbol	Accession Number
HSPA8	0.51	0.0261	HSPA8	NM_006597
RPS13	0.58	0.0089	RPS13	NM_001017
RPLPO	0.63	0.0324	RPLP0	NM_001002
NDUFS3	0.66	0.0142	NDUFS3	NM_004551
LMNB1	0.67	0.0202	LMNB1	NM_005573
ST14	0.67	0.0206	ST14	NM_021978
BRCA1	0.68	0.0032	BRCA1	NM_007295
TMSB4X	0.68	0.0075	TMSB4X	NM_021109
DHFR	0.68	0.0356	DHFR	NM_000791
SKP2	0.69	0.0248	SKP2	NM_005983
TCF-1	0.70	0.0015	TCF1	NM_000545
CDC20	0.70	0.0067	CDC20	NM_001255
SLC25A3	0.70	0.0418	SLC25A3	NM_213611
NME1	0.72	0.0503	NME1	NM_000269
RRM1	0.72	0.0850	RRM1	NM_001033
MCM2	0.76	0.0168	MCM2	NM_004526
ABCC6	0.76	0.0445	ABCC6	NM_001171
CKS2	0.76	0.0869	CKS2	NM_001827
EPHB2	0.77	0.0174	EPHB2	NM_004442
C20 orf1	0.77	0.0716	TPX2	NM_012112
CSEL1	0.77	0.0725	CSE1L	NM_001316
NFKBp65	0.78	0.0957	RELA	NM_021975
AURKB	0.79	0.0742	AURKB	NM_004217
CMYC	0.82	0.0901	MYC	NM_002467
Cdx2	0.85	0.0510	CDX2	NM_001265
EREG	0.85	0.0730	EREG	NM_001432
AREG	0.86	0.0365	AREG	NM_001657

Table 5A shows associations between gene expression and RFI, controlling for particular demographic and clinical characteristics of patients included in the analysis. All genes are listed whose expression correlates with RFI (p<0.1) and which demonstrated a Hazard Ratio>1 in a multivariate analysis including the following variables: tumor location, surgery, tumor grade, nodes examined, and number of positive nodes.

TABLE 5A

Gene	HR	LR Chi-Square	DF	P-Value
RARB	2.06780	4.23265	1	0.03965
CYP3A4	1.85387	7.99462	1	0.00469
ANXA2	1.80012	10.84166	1	0.00099
COX2	1.79051	4.52307	1	0.03344
RhoC	1.73986	9.97133	1	0.00159
MAPK14	1.68382	8.04253	1	0.00457
UBC	1.67323	11.69444	1	0.00063
RhoB	1.66612	15.92497	1	0.00007
ITGB1	1.65796	8.18638	1	0.00422
KRAS2	1.63873	6.80447	1	0.00909
NTN1	1.61833	5.43469	1	0.01974
ATP5E	1.60990	4.93660	1	0.02629
G-Catenin	1.58482	9.24422	1	0.00236
STC1	1.58163	11.10757	1	0.00086
SPINT2	1.52653	6.17276	1	0.01297
Claudin 4	1.50290	12.29943	1	0.00045
IGFBP7	1.48789	9.62569	1	0.00192
NCAM1	1.48294	5.11428	1	0.02373
TIMP1	1.46045	9.98492	1	0.00158
CEBPB	1.46025	5.23659	1	0.02212
KCNH2 iso a/b	1.44616	3.97304	1	0.04623
TMSB10	1.43107	4.65463	1	0.03097
VEGFC	1.41860	4.66904	1	0.03071
HB-EGF	1.41757	7.00399	1	0.00813
FST	1.41061	5.59674	1	0.01799
LAMC2	1.40860	11.33997	1	0.00076
GADD45B	1.40671	12.26323	1	0.00046
AKT3	1.40161	10.13028	1	0.00146
EFNA1	1.40048	8.86645	1	0.00290
p21	1.39939	5.42981	1	0.01980
INHBA	1.38204	11.03909	1	0.00089
CALD1	1.38009	6.93406	1	0.00846
DUSP1	1.36464	13.04379	1	0.00030
HSPG2	1.36387	4.11749	1	0.04244
GJB2	1.36358	8.42204	1	0.00371
EPAS1	1.36323	4.74318	1	0.02941
BGN	1.35821	7.66947	1	0.00562
TIMP2	1.35571	5.78791	1	0.01614
A-Catenin	1.35566	4.35623	1	0.03687
LOXL2	1.35470	7.23663	1	0.00714
DKK1	1.35126	3.88504	1	0.04872
ITGAV	1.34899	8.03554	1	0.00459
CGB	1.34840	7.06221	1	0.00787
EGR1	1.33424	8.41855	1	0.00371
TIMP3	1.33197	6.28550	1	0.01217
VIM	1.33196	4.92198	1	0.02652
TGFBI	1.32511	8.30278	1	0.00396
FXYD5	1.32500	6.22751	1	0.01258
VEGF	1.32291	4.93825	1	0.02627
ADAMTS12	1.31794	7.46749	1	0.00628
SLPI	1.31565	8.38324	1	0.00379
DLC1	1.30862	5.51638	1	0.01884
HOXB7	1.30822	8.04076	1	0.00457
TMEPAI	1.30395	8.43736	1	0.00368
IGFBP5	1.30260	5.44022	1	0.01968
CDC42BPA	1.30167	4.20771	1	0.04024
PDGFA	1.29760	5.54964	1	0.01848
GSTp	1.29594	3.96268	1	0.04652
FOS	1.29427	8.42847	1	0.00369
PDGFC	1.28813	6.81737	1	0.00903
IGFBP3	1.28701	6.33625	1	0.01183
LOX	1.28433	8.15598	1	0.00429
SPARC	1.28260	4.75876	1	0.02915
EFNB2	1.27720	4.71247	1	0.02994
Maspin	1.27645	10.57657	1	0.00115
THBS1	1.27619	6.61087	1	0.01014
TAGLN	1.26904	5.15123	1	0.02323
VEGF_altsplice1	1.26734	5.29282	1	0.02141
S100P	1.26586	9.88713	1	0.00166
HSPA1A	1.26209	8.59704	1	0.00337
MAD	1.26112	3.96163	1	0.04655
ANGPT2	1.25701	3.91148	1	0.04796
PRKCA	1.24853	4.69452	1	0.03026
F3	1.24848	5.06788	1	0.02437
FAP	1.24657	5.19589	1	0.02264
BRK	1.24507	5.44048	1	0.01968
CD68	1.23943	4.02530	1	0.04482
NR4A1	1.23772	7.09548	1	0.00773
CTHRC1	1.23465	5.21100	1	0.02244
SLC2A1	1.22967	5.22364	1	0.02228
Grb10	1.22209	4.12811	1	0.04218
p16-INK4	1.21325	4.44296	1	0.03505
MDK	1.21116	5.25025	1	0.02194
CYR61	1.19995	4.14452	1	0.04177
LAMA3	1.19794	4.33073	1	0.03743
FOXO3A	1.19557	4.20079	1	0.04041
EFNA3	1.19439	5.51728	1	0.01883
CRYAB	1.17514	3.90435	1	0.04816
CEACAM6	1.16804	3.96486	1	0.04646
OPN_osteopontin	1.16112	5.50891	1	0.01892
KLK10	1.15851	5.65625	1	0.01739
SFRP2	1.15773	4.02893	1	0.04473
KLK6	1.15163	4.65953	1	0.03088
S100A2	1.14185	3.94284	1	0.04707
REG4	1.09037	4.16995	1	0.04115

Table 5B shows associations between gene expression and RFI, controlling for particular demographic and clinical characteristics of patients included in the analysis. All genes are listed whose expression correlates with RFI (p<0.1) and which demonstrated a Hazard Ratio<1 in a multivariate analysis including the following variables: tumor location, surgery, tumor grade, nodes examined, and number of positive nodes.

TABLE 5B

Gene	HR	LR Chi-Square	DF	P-Value
BFGF	0.46674	6.95233	1	0.00837
Fasl	0.47324	4.08714	1	0.04321
KLRK1	0.63331	10.28820	1	0.00134
DHFR	0.64947	7.64434	1	0.00570
BRCA1	0.65247	15.21566	1	0.00010
SLC25A3	0.67480	5.72977	1	0.01668
RAD54L	0.68215	5.38684	1	0.02029
PPM1D	0.68777	10.02879	1	0.00154
CD80	0.69347	8.70087	1	0.00318
ATP5A1	0.70467	4.06718	1	0.04372
PRKCB1	0.73152	5.21950	1	0.02234
KIF22	0.73945	5.13202	1	0.02349
Chk1	0.75865	4.38139	1	0.03633
TRAIL	0.76430	4.12533	1	0.04225
CDC20	0.77071	5.04557	1	0.02469
DUT	0.78196	4.13381	1	0.04203
ABCB1	0.79434	5.33783	1	0.02087
UMPS	0.80011	4.65425	1	0.03098
ING5	0.80230	4.04085	1	0.04441
CMYC	0.80757	4.26709	1	0.03886
CBP1	0.83015	3.98302	1	0.04596
AREG	0.86091	4.94239	1	0.02621

Table 6 shows associations between gene expression and clinical outcome based on a nonlinear proportional hazards analysis, using a 2 degree-of-freedom natural spline. All genes are listed which demonstrated a departure from a strictly linear relationship ($p<0.05$) with RFI in combined Stage II (Duke's B) and Stage III (Duke's C) patients. The relationship between gene expression and RFI was not constant throughout the observed range of expression values in the study, e.g. increases in gene expression may have been related to increases in duration of RFI in one portion of the observed range and with decreases in duration of RFI in a different portion of the range.

TABLE 6

Gene	P-Value	Official Symbol	Accession Number
PTHLH	0.001	PTHLH	NM_002820
CDCA7 v2	0.002	CDCA7	NM_145810
CREBBP	0.002	CREBBP	NM_004380
KLF5	0.002	KLF5	NM_001730
LAMB3	0.004	LAMB3	NM_000228
TGFBR1	0.005	TGFBR1	NM_004612
NR4A1	0.005	NR4A1	NM_002135
Upa	0.005	PLAU	NM_002658
Cad17	0.007	CDH17	NM_004063
S100A4	0.008	S100A4	NM_002961
A-Catenin	0.008	CTNNA1	NM_001903
EPHB2	0.009	EPHB2	NM_004442
Axin 2	0.011	AXIN2	NM_004655
PTPRJ	0.011	PTPRJ	NM_002843
CAPN1	0.012	CAPN1	NM_005186
CEGP1	0.013	SCUBE2	NM_020974
APOC1	0.013	APOC1	NM_001645
GBP1	0.015	GBP1	NM_002053
SKP2	0.016	SKP2	NM_005983
ATP5E	0.016	ATP5E	NM_006886
GRIK1	0.017	GRIK1	NM_000830
PRKR	0.018	EIF2AK2	NM_002759
FUT6	0.020	FUT6	NM_000150
PFN2	0.020	PFN2	NM_053024
ITGB4	0.021	ITGB4	NM_000213
MADH7	0.021	SMAD7	NM_005904
RALBP1	0.021	RALBP1	NM_006788
AKT1	0.022	AKT1	NM_005163
KLK6	0.022	KLK6	NM_002774
PLK	0.023	PLK1	NM_005030
CYP2C8	0.025	CYP2C8	NM_000770
BTF3	0.026	BTF3	NM_001207
CCNE2 variant 1	0.026	CCNE2	NM_057749
STMY3	0.030	MMP11	NM_005940
NRP1	0.030	NRP1	NM_003873
SIAT4A	0.031	ST3GAL1	NM_003033
SEMA3B	0.033	SEMA3B	NM_004636
TRAG3	0.033	CSAG2	NM_004909
HSPE1	0.035	HSPE1	NM_002157
SBA2	0.036	WSB2	NM_018639
TK1	0.036	TK1	NM_003258
CCNB2	0.037	CCNB2	NM_004701
TMEPAI	0.037	TMEPAI	NM_020182
SPRY2	0.037	SPRY2	NM_005842
AGXT	0.038	AGXT	NM_000030
ALCAM	0.038	ALCAM	NM_001627
HSPCA	0.038	HSPCA	NM_005348
TIMP3	0.038	TIMP3	NM_000362
DET1	0.039	DET1	NM_017996
tusc4	0.040	TUSC4	NM_006545
SNAI2	0.040	SNAI2	NM_003068
CD28	0.040	CD28	NM_006139
RNF11	0.041	RNF11	NM_014372
PAI1	0.042	SERPINE1	NM_000602
XRCC1	0.042	XRCC1	NM_006297
EGLN1	0.044	EGLN1	NM_022051
EGFR	0.044	EGFR	NM_005228
HES6	0.044	HES6	NM_018645
KCNK4	0.045	KCNK4	NM_016611
CXCR4	0.047	CXCR4	NM_003467
PTP4A3	0.048	PTP4A3	NM_007079
p27	0.048	CDKN1B	NM_004064
MADH4	0.049	SMAD4	NM_005359
ICAM1	0.049	ICAM1	NM_000201

Table 7 shows all genes exhibiting an interaction (p-value<0.05) with tumor stage. The data were modeled using a proportional hazards model of RFI with gene expression, tumor stage, and their interaction as predictors.

TABLE 7

Gene	HR Stage II	HR Stage III	P-value for Interaction
ICAM2	1.49	0.68	0.0019
CD24	1.26	0.84	0.0054
PRDX6	2.29	0.73	0.0058
HSD17B2	0.62	1.29	0.0072
ALCAM	1.61	0.94	0.0088
SIR2	2.02	1.09	0.0089
NUFIP1	1.32	0.79	0.0093
EMR3	2.14	0.57	0.0127
CDC20	0.56	0.98	0.0130
MT3	1.37	0.79	0.0134
CLTC	1.80	0.71	0.0144
CYR61	1.73	1.10	0.0145
WIF	1.34	0.78	0.0195
TFF3	1.23	0.90	0.0209
SOS1	1.46	0.79	0.0287
TMSB4X	1.34	0.74	0.0293
CENPE	3.05	0.85	0.0330
CDH11	1.49	0.96	0.0339
CAPG	0.90	1.50	0.0348
TP53BP1	1.54	0.93	0.0357
MGAT5	1.25	0.73	0.0362
MADH2	1.36	0.70	0.0393
LOX	1.58	1.11	0.0396
DKK1	0.87	1.55	0.0415
CKS1B	0.31	1.75	0.0467
MMP7	0.92	1.28	0.0471
STAT5B	1.28	0.86	0.0471
CD28	0.69	1.25	0.0472

Second Analysis Study Results

Reference Gene Set for the second analysis was ATP5E, CLTC, GPX1, NEDD8, PGK1, UBB.

Table 1.2A shows associations for those genes whose increased expression is predictive of shorter Recurrence-Free Interval (RFI) based on univariate proportional hazards analysis.

Table 1.2B shows associations for those genes whose increased expression is predictive of longer Recurrence-Free Interval (RFI) based on univariate proportional hazards analysis.

Table 2.2A shows associations for those genes whose increased expression is predictive of decreased rate of Overall Survival (OS) based on univariate proportional hazards analysis.

Table 2.2B shows associations for those genes whose increased expression is predictive of increased rate of Overall Survival (OS) based on univariate proportional hazards analysis.

Table 3.2A shows associations for those genes whose increased expression is predictive of decreased rate of Disease Free Survival (DFS) based on univariate proportional hazards analysis.

Table 3.2B shows associations for those genes whose increased expression is predictive of increased rate of Disease Free Survival (DFS) based on univariate proportional hazards analysis.

Table 4.2A shows associations for those genes whose increased expression is predictive of shorter Distant Recurrence-Free Interval (DRFI) based on univariate proportional hazards analysis.

Table 4.2B shows associations for those genes whose increased expression is predictive of longer Distant Recurrence-Free Interval (DRFI) based on univariate proportional hazards analysis.

Table 5.2A shows associations between gene expression and RFI for those genes whose increased expression is predictive of shorter Recurrence-Free Interval (RFI), based on a multivariate analysis controlling for particular demographic and clinical characteristics of patients included in the analysis.

Table 5.2B shows associations between gene expression and RFI for those genes whose increased expression is predictive of longer Recurrence-Free Interval (RFI), based on a multivariate analysis controlling for particular demographic and clinical characteristics of patients included in the analysis.

Table 6.2 shows genes for which an association between gene expression and clinical outcome was identified based on a nonlinear proportional hazards analysis, using a 2 degree-of-freedom natural spline.

Table 7.2 shows all genes exhibiting an interaction (p-value<0.05) with tumor stage.

Table 1.2A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using RFI as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
RARB	2.22	0.0294	RARB	NM_016152
ITGB1	2.04	0.0002	ITGB1	NM_002211
ANXA2	1.78	0.0003	ANXA2	NM_004039
CYP3A4	1.68	0.0075	CYP3A4	NM_017460
COX2	1.64	0.0604	PTGS2	NM_000963
KRAS2	1.62	0.0064	KRAS	NM_004985
TJP1	1.58	0.0751	TJP1	NM_003257
KIAA0125	1.58	0.0889	KIAA0125	NM_014792
RhoB	1.57	0.0002	RHOB	NM_004040
RhoC	1.56	0.0059	RHOC	NM_175744
NTN1	1.54	0.0336	NTN1	NM_004822
ANXA5	1.52	0.0086	ANXA5	NM_001154
TIMP1	1.52	<.0001	TIMP1	NM_003254
AKT3	1.50	<.0001	AKT3	NM_005465
CALD1	1.48	0.0007	CALD1	NM_004342
IGFBP7	1.46	0.0023	IGFBP7	NM_001553
CYP1B1	1.45	0.0222	CYP1B1	NM_000104
BGN	1.44	0.0002	BGN	NM_001711
VEGFC	1.44	0.0151	VEGFC	NM_005429
DLC1	1.44	0.0014	DLC1	NM_006094
SI	1.42	0.0086	SI	NM_001041
TIMP2	1.42	0.0022	TIMP2	NM_003255
CDC42BPA	1.41	0.0038	CDC42BPA	NM_003607
LAMC2	1.40	0.0004	LAMC2	NM_005562
ITGAV	1.40	0.0019	ITGAV	NM_002210
CTSB	1.40	0.0357	CTSB	NM_001908
DUSP1	1.39	<.0001	DUSP1	NM_004417
TLN1	1.39	0.0335	TLN1	NM_006289
CCNE2 variant 1	1.39	0.0708	CCNE2	NM_057749
TIMP3	1.38	0.0023	TIMP3	NM_000362
GHI BRAF mut4	1.38	0.0537		GHI_BRAF_mut4
HB-EGF	1.38	0.0109	HBEGF	NM_001945
HSPG2	1.38	0.0258	HSPG2	NM_005529
VIM	1.37	0.0077	VIM	NM_003380
ROCK1	1.37	0.0168	ROCK1	NM_005406
S100A1	1.36	0.0233	S100A1	NM_006271
p21	1.36	0.0113	CDKN1A	NM_000389
CGB	1.36	0.0023	CGB	NM_000737
UBC	1.36	0.0137	UBC	NM_021009
GADD45B	1.36	0.0003	GADD45B	NM_015675
INHBA	1.35	0.0010	INHBA	NM_002192
VCL	1.34	0.0286	VCL	NM_003373
SIR2	1.34	0.0049	SIRT1	NM_012238
CD68	1.34	0.0042	CD68	NM_001251
Maspin	1.34	<.0001	SERPINB5	NM_002639
FST	1.33	0.0326	FST	NM_006350
EPAS1	1.33	0.0306	EPAS1	NM_001430
LOXL2	1.33	0.0076	LOXL2	NM_002318
STC1	1.33	0.0119	STC1	NM_003155
UNC5C	1.32	0.0642	UNC5C	NM_003728
IGFBP5	1.32	0.0080	IGFBP5	NM_000599
INHBB	1.32	0.0643	INHBB	NM_002193
FAP	1.32	0.0017	FAP	NM_004460
DKK1	1.31	0.0298	DKK1	NM_012242
FYN	1.31	0.0053	FYN	NM_002037
CTHRC1	1.31	0.0017	CTHRC1	NM_138455
FOS	1.31	0.0010	FOS	NM_005252
RBX1	1.31	0.0633	RBX1	NM_014248
TAGLN	1.31	0.0058	TAGLN	NM_003186
SBA2	1.31	0.0439	WSB2	NM_018639
CYR61	1.30	0.0018	CYR61	NM_001554
SPARC	1.30	0.0117	SPARC	NM_003118
SNAI2	1.30	0.0076	SNAI2	NM_003068
TMSB10	1.30	0.0757	TMSB10	NM_021103
IGFBP3	1.30	0.0056	IGFBP3	NM_000598
PDGFC	1.29	0.0040	PDGFC	NM_016205
SLPI	1.29	0.0026	SLPI	NM_003064
COL1A2	1.29	0.0087	COL1A2	NM_000089
NRP2	1.29	0.0112	NRP2	NM_003872
PRKCA	1.29	0.0093	PRKCA	NM_002737
KLF6	1.29	0.0661	KLF6	NM_001300
THBS1	1.28	0.0062	THBS1	NM_003246
EGR1	1.28	0.0067	EGR1	NM_001964
S100A4	1.28	0.0070	S100A4	NM_002961
CXCR4	1.28	0.0089	CXCR4	NM_003467
LAMA3	1.27	0.0024	LAMA3	NM_000227

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Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
LOX	1.26	0.0036	LOX	NM_002317
AKAP12	1.26	0.0046	AKAP12	NM_005100
ADAMTS12	1.26	0.0109	ADAMTS12	NM_030955
MCP1	1.25	0.0122	CCL2	NM_002982
Grb10	1.25	0.0107	GRB10	NM_005311
PTGER3	1.25	0.0240	PTGER3	NM_000957
CRYAB	1.25	0.0035	CRYAB	NM_001885
ANGPT2	1.25	0.0566	ANGPT2	NM_001147
ANXA1	1.25	0.0353	ANXA1	NM_000700
EphB6	1.24	0.0960	EPHB6	NM_004445
PDGFB	1.24	0.0139	PDGFB	NM_002608
COL1A1	1.24	0.0198	COL1A1	NM_000088
TGFB3	1.23	0.0094	TGFB3	NM_003239
CTGF	1.23	0.0265	CTGF	NM_001901
PDGFA	1.23	0.0312		NM_002607
HSPA1A	1.23	0.0027	HSPA1A	NM_005345
EFNB2	1.23	0.0331	EFNB2	NM_004093
CAPG	1.23	0.0724	CAPG	NM_001747
TGFBI	1.22	0.0231	TGFBI	NM_000358
SIAT4A	1.22	0.0253	ST3GAL1	NM_003033
LAT	1.22	0.0307	LAT	NM_014387
ITGA5	1.22	0.0224	ITGA5	NM_002205
GBP2	1.22	0.0225	GBP2	NM_004120
ANTXR1	1.22	0.0204	ANTXR1	NM_032208
ID4	1.22	0.0512	ID4	NM_001546
SFRP2	1.22	0.0039	SFRP2	NM_003013
TMEPAI	1.21	0.0170	TMEPAI	NM_020182
CTSL	1.21	0.0388	CTSL	NM_001912
KLK10	1.21	0.0007	KLK10	NM_002776
FXYD5	1.21	0.0547	FXYD5	NM_014164
GJB2	1.21	0.0356	GJB2	NM_004004
P14ARF	1.21	0.0451		S78535
DAPK1	1.21	0.0525	DAPK1	NM_004938
SKP1A	1.21	0.0663	SKP1A	NM_006930
SFRP4	1.21	0.0078	SFRP4	NM_003014
KLK6	1.20	0.0048	KLK6	NM_002774
GJA1	1.20	0.0345	GJA1	NM_000165
HOXB7	1.20	0.0278	HOXB7	NM_004502
NDRG1	1.20	0.0948	NDRG1	NM_006096
PAI1	1.19	0.0061	SERPINE1	NM_000602
CDH11	1.19	0.0762	CDH11	NM_001797
EGR3	1.19	0.0149	EGR3	NM_004430
EMP1	1.19	0.0533	EMP1	NM_001423
FZD1	1.19	0.0671	FZD1	NM_003505
ABCC5	1.19	0.0631	ABCC5	NM_005688
S100P	1.18	0.0160	S100P	NM_005980
OPN, osteopontin	1.18	0.0030	SPP1	NM_000582
p16-INK4	1.17	0.0503		L27211
NR4A1	1.17	0.0332	NR4A1	NM_002135
TUBB	1.17	0.0950	TUBB2	NM_001069
SIAT7B	1.17	0.0352	ST6GALNAC2	NM_006456
ALDH1A1	1.17	0.0299	ALDH1A1	NM_000689
F3	1.16	0.0654	F3	NM_001993
SLC2A1	1.15	0.0806	SLC2A1	NM_006516
CXCL12	1.13	0.0986	CXCL12	NM_000609
STMY3	1.13	0.0518	MMP11	NM_005940
S100A2	1.13	0.0303	S100A2	NM_005978
FABP4	1.13	0.0363	FABP4	NM_001442
REG4	1.11	0.0034	REG4	NM_032044
pS2	1.09	0.0690	TFF1	NM_003225
MUC2	1.06	0.0674	MUC2	NM_002457

Table 1.2B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using RFI as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
ORC1L	0.41	0.0623	ORC1L	NM_004153
E2F1	0.63	0.0006	E2F1	NM_005225
HSPA8	0.63	0.0346	HSPA8	NM_006597
RAD54L	0.65	0.0026	RAD54L	NM_003579
BRCA1	0.68	0.0001	BRCA1	NM_007295
SLC25A3	0.70	0.0100	SLC25A3	NM_213611
PPM1D	0.71	0.0025	PPM1D	NM_003620
DHFR	0.71	0.0106	DHFR	NM_000791
SKP2	0.72	0.0087	SKP2	NM_005983
FASN	0.73	0.0070	FASN	NM_004104
HNRPD	0.73	0.0611	HNRPD	NM_031370
ENO1	0.74	0.0432	ENO1	NM_001428
C20 orf1	0.74	0.0086	TPX2	NM_012112
BRCA2	0.75	0.0515	BRCA2	NM_000059
DDB1	0.75	0.0639	DDB1	NM_001923
KIF22	0.76	0.0127	KIF22	NM_007317
RPLPO	0.76	0.0330	RPLP0	NM_001002
Chk1	0.76	0.0164	CHEK1	NM_001274
ST14	0.77	0.0392	ST14	NM_021978
Bax	0.77	0.0502	BAX	NM_004324
TCF-1	0.78	0.0023	TCF1	NM_000545
LMNB1	0.78	0.0458	LMNB1	NM_005573
RRM1	0.78	0.0693	RRM1	NM_001033
CSEL1	0.79	0.0261	CSE1L	NM_001316
CDC20	0.79	0.0274	CDC20	NM_001255
PRDX2	0.79	0.0930	PRDX2	NM_005809
RPS13	0.79	0.0906	RPS13	NM_001017
RAF1	0.80	0.0717	RAF1	NM_002880
CMYC	0.80	0.0095	MYC	NM_002467
UBE2M	0.80	0.0390	UBE2M	NM_003969
CKS2	0.80	0.0596	CKS2	NM_001827
NME1	0.80	0.0694	NME1	NM_000269
c-myb (MYB official)	0.80	0.0082	MYB	NM_005375
CD80	0.80	0.0688	CD80	NM_005191
CDCA7 v2	0.81	0.0164	CDCA7	NM_145810
EFP	0.81	0.0387	TRIM25	NM_005082
CCNE2	0.81	0.0405	CCNE2	NM_057749
SURV	0.81	0.0573	BIRC5	NM_001168
RRM2	0.82	0.0181	RRM2	NM_001034
ABCC6	0.82	0.0464	ABCC6	NM_001171
UMPS	0.82	0.0371	UMPS	NM_000373
PI3KC2A	0.82	0.0855	PIK3C2A	NM_002645
NOTCH1	0.82	0.0222	NOTCH1	NM_017617
EIF4E	0.82	0.0928	EIF4E	NM_001968
EPHB2	0.82	0.0183	EPHB2	NM_004442
AREG	0.83	0.0012	AREG	NM_001657
EREG	0.83	0.0059	EREG	NM_001432
MYBL2	0.83	0.0234	MYBL2	NM_002466
ABCB1	0.83	0.0342	ABCB1	NM_000927
HRAS	0.83	0.0708	HRAS	NM_005343
SLC7A5	0.84	0.0547	SLC7A5	NM_003486
MAD2L1	0.84	0.0653	MAD2L1	NM_002358
ING5	0.85	0.0920	ING5	NM_032329
Ki-67	0.85	0.0562	MKI67	NM_002417
MCM2	0.85	0.0671	MCM2	NM_004526
Cdx2	0.88	0.0430	CDX2	NM_001265
HES6	0.89	0.0966	HES6	NM_018645
PTPRO	0.89	0.0664	PTPRO	NM_030667
cripto (TDGF1 official)	0.90	0.0781	TDGF1	NM_003212

Table 2.2A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using OS as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
RhoC	1.66	0.0002	RHOC	NM_175744
ITGB1	1.59	0.0049	ITGB1	NM_002211
ANXA2	1.58	0.0004	ANXA2	NM_004039
CYP3A4	1.49	0.0114	CYP3A4	NM_017460
p21	1.49	<.0001	CDKN1A	NM_000389
HMLH	1.42	0.0555	MLH1	NM_000249
VEGFC	1.41	0.0095	VEGFC	NM_005429
TGFBR1	1.40	0.0113	TGFBR1	NM_004612
UBC	1.38	0.0013	UBC	NM_021009
RhoB	1.37	0.0016	RHOB	NM_004040
HSPG2	1.37	0.0111	HSPG2	NM_005529
PFN1	1.35	0.0987	PFN1	NM_005022
TIMP1	1.35	0.0008	TIMP1	NM_003254
VCL	1.33	0.0116	VCL	NM_003373
INHBB	1.32	0.0265	INHBB	NM_002193
SPINT2	1.32	0.0358	SPINT2	NM_021102
GHI BRAF mut4	1.31	0.0822		GHI_BRAF_mut4
LAMC2	1.31	0.0007	LAMC2	NM_005562
KCNH2 iso a/b	1.31	0.0474	KCNH2	NM_000238
UNC5C	1.30	0.0417	UNC5C	NM_003728
CDC42	1.30	0.0122	CDC42	NM_001791
UBL1	1.29	0.0169	SUMO1	NM_003352
GADD45B	1.29	0.0003	GADD45B	NM_015675
KRAS2	1.29	0.0774	KRAS	NM_004985
HB-EGF	1.29	0.0219	HBEGF	NM_001945
DKK1	1.28	0.0304	DKK1	NM_012242
FXYD5	1.28	0.0035	FXYD5	NM_014164
CALD1	1.28	0.0107	CALD1	NM_004342
ANXA5	1.27	0.0723	ANXA5	NM_001154
HLA-G	1.27	0.0732	HLA-G	NM_002127
DUSP1	1.27	0.0004	DUSP1	NM_004417
LOXL2	1.27	0.0050	LOXL2	NM_002318
CDC42BPA	1.27	0.0155	CDC42BPA	NM_003607
BGN	1.27	0.0039	BGN	NM_001711
LAMB3	1.27	0.0221	LAMB3	NM_000228
EphB6	1.27	0.0373	EPHB6	NM_004445
SHC1	1.27	0.0582	SHC1	NM_003029
TIMP2	1.26	0.0126	TIMP2	NM_003255
CTSB	1.26	0.0748	CTSB	NM_001908
TIMP3	1.26	0.0072	TIMP3	NM_000362
ID3	1.26	0.0033	ID3	NM_002167
CAPG	1.26	0.0162	CAPG	NM_001747
NRP1	1.26	0.0135	NRP1	NM_003873
INHBA	1.26	0.0021	INHBA	NM_002192
KLF6	1.25	0.0477	KLF6	NM_001300
IGFBP7	1.25	0.0251	IGFBP7	NM_001553
S100A1	1.25	0.0528	S100A1	NM_006271
EPAS1	1.24	0.0382	EPAS1	NM_001430
DLC1	1.24	0.0228	DLC1	NM_006094
KLK10	1.24	<.0001	KLK10	NM_002776
SBA2	1.24	0.0493	WSB2	NM_018639
SPARC	1.24	0.0133	SPARC	NM_003118
GAGE4	1.23	0.0475	GAGE4	NM_001474
HSPA1A	1.23	0.0004	HSPA1A	NM_005345
SIR2	1.23	0.0179	SIRT1	NM_012238
CGB	1.23	0.0202	CGB	NM_000737
Grb10	1.22	0.0059	GRB10	NM_005311
SNAI2	1.22	0.0145	SNAI2	NM_003068
LAMA3	1.22	0.0019	LAMA3	NM_000227
AKT3	1.22	0.0169	AKT3	NM_005465
FYN	1.22	0.0138	FYN	NM_002037
FOS	1.22	0.0035	FOS	NM_005252
CTHRC1	1.21	0.0056	CTHRC1	NM_138455
CTSD	1.21	0.0506	CTSD	NM_001909
THY1	1.21	0.0290	THY1	NM_006288
ANXA1	1.21	0.0339	ANXA1	NM_000700
CD68	1.21	0.0227	CD68	NM_001251
G-Catenin	1.20	0.0789	JUP	NM_002230
PLK3	1.20	0.0081	PLK3	NM_004073
STC1	1.20	0.0577	STC1	NM_003155
TAGLN	1.20	0.0238	TAGLN	NM_003186
VIM	1.20	0.0632	VIM	NM_003380
HSPA1B	1.20	0.0302	HSPA1B	NM_005346
LAT	1.20	0.0184	LAT	NM_014387
KRT19	1.20	0.0309	KRT19	NM_002276
IGFBP3	1.20	0.0167	IGFBP3	NM_000598
BMP4	1.20	0.0035	BMP4	NM_001202
KLK6	1.20	0.0014	KLK6	NM_002774
THBS1	1.20	0.0206	THBS1	NM_003246
TULP3	1.19	0.0344	TULP3	NM_003324
ERK1	1.19	0.0522		Z11696
CREBBP	1.19	0.0866	CREBBP	NM_004380
S100A4	1.19	0.0259	S100A4	NM_002961
PDGFB	1.19	0.0205	PDGFB	NM_002608
EFNB2	1.19	0.0299	EFNB2	NM_004093
LOX	1.19	0.0104	LOX	NM_002317
PTK2	1.18	0.0983	PTK2	NM_005607
IGFBP5	1.18	0.0544	IGFBP5	NM_000599
APC	1.18	0.0461	APC	NM_000038
DYRK1B	1.18	0.0681	DYRK1B	NM_004714
NOTCH2	1.18	0.0533	NOTCH2	NM_024408
Maspin	1.18	0.0033	SERPINB5	NM_002639
AKAP12	1.18	0.0195	AKAP12	NM_005100
COL1A1	1.17	0.0417	COL1A1	NM_000088
EMP1	1.17	0.0295	EMP1	NM_001423
SIAT4A	1.17	0.0311	ST3GAL1	NM_003033
PAI1	1.17	0.0036	SERPINE1	NM_000602
NR4A1	1.17	0.0117	NR4A1	NM_002135
EGR1	1.17	0.0379	EGR1	NM_001964
BRK	1.17	0.0156	PTK6	NM_005975
UNC5B	1.17	0.0956	UNC5B	NM_170744
SR-A1	1.17	0.0512	SR-A1	NM_021228
MRP3	1.16	0.0353	ABCC3	NM_003786
hCRA a	1.16	0.0878		U78556
Upa	1.16	0.0630	PLAU	NM_002658
BCAS1	1.16	0.0147	BCAS1	NM_003657
PDGFC	1.16	0.0375	PDGFC	NM_016205
COL1A2	1.16	0.0620	COL1A2	NM_000089
CTGF	1.16	0.0580	CTGF	NM_001901
MCP1	1.16	0.0463	CCL2	NM_002982
RAB32	1.16	0.0686	RAB32	NM_006834
SKP1A	1.16	0.0842	SKP1A	NM_006930
FAP	1.16	0.0443	FAP	NM_004460
EFNA1	1.16	0.0990	EFNA1	NM_004428
HOXB7	1.15	0.0378	HOXB7	NM_004502
CYR61	1.15	0.0452	CYR61	NM_001554
TGFBI	1.15	0.0591	TGFBI	NM_000358
TMEPAI	1.15	0.0419	TMEPAI	NM_020182
SIN3A	1.15	0.0853	SIN3A	NM_015477
S100A2	1.15	0.0038	S100A2	NM_005978
PDGFA	1.15	0.0840		NM_002607
MMP7	1.15	0.0469	MMP7	NM_002423
ANTXR1	1.15	0.0520	ANTXR1	NM_032208
SLPI	1.14	0.0755	SLPI	NM_003064
SFRP2	1.13	0.0253	SFRP2	NM_003013
S100A8	1.13	0.0795	S100A8	NM_002964
TP53I3	1.13	0.0973	TP53I3	NM_004881
F3	1.13	0.0735	F3	NM_001993
OPN, osteopontin	1.12	0.0100	SPP1	NM_000582
EGLN3	1.11	0.0883	EGLN3	NM_022073
FZD6	1.11	0.0791	FZD6	NM_003506
OSM	1.10	0.0913	OSM	NM_020530
FABP4	1.10	0.0521	FABP4	NM_001442
GSTT1	1.09	0.0837	GSTT1	NM_000853
REG4	1.07	0.0300	REG4	NM_032044

Table 2.2B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using OS as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
ORC1L	0.52	0.0895	ORC1L	NM_004153
HSPA8	0.64	0.0164	HSPA8	NM_006597

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Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
SKP2	0.71	0.0012	SKP2	NM_005983
PRDX4	0.74	0.0202	PRDX4	NM_006406
DHFR	0.76	0.0111	DHFR	NM_000791
FGF18	0.76	0.0915	FGF18	NM_003862
SLC25A3	0.76	0.0391	SLC25A3	NM_213611
RRM1	0.77	0.0218	RRM1	NM_001033
E2F1	0.78	0.0180	E2F1	NM_005225
SURV	0.79	0.0098	BIRC5	NM_001168
PPM1D	0.80	0.0154	PPM1D	NM_003620
CCNE2	0.80	0.0090	CCNE2	NM_057749
BRCA1	0.80	0.0093	BRCA1	NM_007295
ST14	0.80	0.0436	ST14	NM_021978
c-myb (MYB official)	0.81	0.0027	MYB	NM_005375
Chk1	0.81	0.0220	CHEK1	NM_001274
C20 orf1	0.81	0.0305	TPX2	NM_012112
EI24	0.81	0.0574	EI24	NM_004879
CDC20	0.82	0.0234	CDC20	NM_001255
TCF-1	0.82	0.0061	TCF1	NM_000545
PPID	0.83	0.0584	PPID	NM_005038
KIF22	0.83	0.0466	KIF22	NM_007317
UBE2M	0.83	0.0850	UBE2M	NM_003969
MRPL40	0.83	0.0716	MRPL40	NM_003776
RPLPO	0.84	0.0987	RPLP0	NM_001002
LMNB1	0.84	0.0910	LMNB1	NM_005573
DUT	0.84	0.0401	DUT	NM_001948
CD44E	0.84	0.0483		X55150
MCM2	0.85	0.0214	MCM2	NM_004526
CDC6	0.85	0.0235	CDC6	NM_001254
AURKB	0.85	0.0373	AURKB	NM_004217
SMARCA3	0.86	0.0562	SMARCA3	NM_003071
CDCA7 v2	0.86	0.0435	CDCA7	NM_145810
EPHB2	0.86	0.0281	EPHB2	NM_004442
CMYC	0.86	0.0441	MYC	NM_002467
ABCB1	0.86	0.0352	ABCB1	NM_000927
Cdx2	0.87	0.0156	CDX2	NM_001265
PPARG	0.88	0.0655	PPARG	NM_005037
MYBL2	0.88	0.0667	MYBL2	NM_002466
EREG	0.89	0.0352	EREG	NM_001432
AREG	0.90	0.0221	AREG	NM_001657

Table 3.2A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DFS as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
ANXA2	1.67	<.0001	ANXA2	NM_004039
CYP3A4	1.59	0.0035	CYP3A4	NM_017460
RhoC	1.52	0.0010	RHOC	NM_175744
TJP1	1.44	0.0951	TJP1	NM_003257
HB-EGF	1.39	0.0023	HBEGF	NM_001945
p21	1.39	0.0006	CDKN1A	NM_000389
HMLH	1.37	0.0678	MLH1	NM_000249
ITGB1	1.37	0.0419	ITGB1	NM_002211
UBC	1.34	0.0024	UBC	NM_021009
VEGFC	1.33	0.0246	VEGFC	NM_005429
TIMP1	1.33	0.0007	TIMP1	NM_003254
CCNE2 variant 1	1.32	0.0745	CCNE2	NM_057749
SPINT2	1.32	0.0224	SPINT2	NM_021102
LAMC2	1.32	0.0002	LAMC2	NM_005562
VCL	1.31	0.0119	VCL	NM_003373
RhoB	1.31	0.0049	RHOB	NM_004040
PKR2	1.30	0.0258	PKM2	NM_002654
ANXA5	1.30	0.0406	ANXA5	NM_001154
GADD45B	1.30	0.0001	GADD45B	NM_015675
INHBB	1.29	0.0368	INHBB	NM_002193
DUSP1	1.29	<.0001	DUSP1	NM_004417

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Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
KRAS2	1.28	0.0686	KRAS	NM_004985
KLF6	1.28	0.0284	KLF6	NM_001300
IGFBP7	1.27	0.0103	IGFBP7	NM_001553
GRIK1	1.27	0.0421	GRIK1	NM_000830
DLC1	1.27	0.0084	DLC1	NM_006094
FOS	1.26	0.0003	FOS	NM_005252
HSPG2	1.26	0.0443	HSPG2	NM_005529
INHBA	1.26	0.0009	INHBA	NM_002192
TIMP3	1.26	0.0045	TIMP3	NM_000362
BGN	1.26	0.0035	BGN	NM_001711
CGB	1.26	0.0172	CGB	NM_000737
HK1	1.26	0.0352	HK1	NM_000188
SHC1	1.25	0.0562	SHC1	NM_003029
STC1	1.25	0.0161	STC1	NM_003155
LOXL2	1.24	0.0078	LOXL2	NM_002318
CAPG	1.24	0.0161	CAPG	NM_001747
UNC5B	1.23	0.0204	UNC5B	NM_170744
MVP	1.23	0.0729	MVP	NM_017458
CTSD	1.23	0.0256	CTSD	NM_001909
EGR1	1.23	0.0041	EGR1	NM_001964
LOX	1.23	0.0017	LOX	NM_002317
CDC42BPA	1.23	0.0278	CDC42BPA	NM_003607
GAGE4	1.23	0.0425	GAGE4	NM_001474
CALD1	1.22	0.0239	CALD1	NM_004342
FXYD5	1.22	0.0096	FXYD5	NM_014164
EphB6	1.22	0.0825	EPHB6	NM_004445
LAMB3	1.22	0.0444	LAMB3	NM_000228
VEGF	1.21	0.0267	VEGF	NM_003376
PDGFB	1.21	0.0062	PDGFB	NM_002608
TIMP2	1.21	0.0292	TIMP2	NM_003255
A-Catenin	1.21	0.0598	CTNNA1	NM_001903
IGFBP3	1.21	0.0081	IGFBP3	NM_000598
CD68	1.21	0.0138	CD68	NM_001251
S100A1	1.21	0.0886	S100A1	NM_006271
SIAT4A	1.21	0.0076	ST3GAL1	NM_003033
HSPA1B	1.21	0.0182	HSPA1B	NM_005346
DKK1	1.20	0.0900	DKK1	NM_012242
SBA2	1.20	0.0733	WSB2	NM_018639
SIR2	1.20	0.0250	SIRT1	NM_012238
THBS1	1.20	0.0119	THBS1	NM_003246
FYN	1.20	0.0156	FYN	NM_002037
TULP3	1.20	0.0205	TULP3	NM_003324
LAMA3	1.20	0.0026	LAMA3	NM_000227
NR4A1	1.20	0.0022	NR4A1	NM_002135
EFNA1	1.20	0.0258	EFNA1	NM_004428
EMP1	1.20	0.0102	EMP1	NM_001423
SPARC	1.19	0.0333	SPARC	NM_003118
G-Catenin	1.19	0.0761	JUP	NM_002230
CYR61	1.19	0.0103	CYR61	NM_001554
Maspin	1.19	0.0015	SERPINB5	NM_002639
HSPA1A	1.18	0.0018	HSPA1A	NM_005345
PTHR1	1.18	0.0856	PTHR1	NM_000316
EPAS1	1.18	0.0789	EPAS1	NM_001430
Grb10	1.18	0.0173	GRB10	NM_005311
ERK1	1.18	0.0464		Z11696
VIM	1.18	0.0772	VIM	NM_003380
SNAI2	1.18	0.0379	SNAI2	NM_003068
IGFBP5	1.17	0.0492	IGFBP5	NM_000599
CTHRC1	1.17	0.0155	CTHRC1	NM_138455
THY1	1.17	0.0562	THY1	NM_006288
NRP1	1.17	0.0747	NRP1	NM_003873
PTGER3	1.17	0.0493	PTGER3	NM_000957
ID3	1.17	0.0437	ID3	NM_002167
F3	1.17	0.0157	F3	NM_001993
CTGF	1.17	0.0394	CTGF	NM_001901
KRT19	1.17	0.0517	KRT19	NM_002276
PAI1	1.17	0.0033	SERPINE1	NM_000602
FAP	1.17	0.0260	FAP	NM_004460
ANXA1	1.16	0.0688	ANXA1	NM_000700
KLK10	1.16	0.0009	KLK10	NM_002776
EFNB2	1.16	0.0447	EFNB2	NM_004093
P14ARF	1.16	0.0573		S78535
MCP1	1.16	0.0359	CCL2	NM_002982
PLK3	1.16	0.0296	PLK3	NM_004073
ANTXR1	1.16	0.0243	ANTXR1	NM_032208
ADAMTS12	1.16	0.0346	ADAMTS12	NM_030955

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Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
EGR3	1.16	0.0109	EGR3	NM_004430
APC	1.16	0.0733	APC	NM_000038
PDGFC	1.16	0.0326	PDGFC	NM_016205
BMP4	1.16	0.0151	BMP4	NM_001202
HOXB7	1.15	0.0281	HOXB7	NM_004502
NDRG1	1.15	0.0912	NDRG1	NM_006096
Herstatin	1.15	0.0380		AF177761
TMEPAI	1.15	0.0268	TMEPAI	NM_020182
IL6	1.15	0.0914	IL6	NM_000600
PDGFA	1.15	0.0599		NM_002607
TGFBI	1.15	0.0439	TGFBI	NM_000358
Upa	1.15	0.0740	PLAU	NM_002658
S100A4	1.15	0.0621	S100A4	NM_002961
SLPI	1.15	0.0447	SLPI	NM_003064
KLK6	1.15	0.0112	KLK6	NM_002774
COL1A1	1.15	0.0637	COL1A1	NM_000088
GJB2	1.15	0.0604	GJB2	NM_004004
PKD1	1.15	0.0939	PKD1	NM_000296
TP53I3	1.15	0.0450	TP53I3	NM_004881
PLAUR	1.14	0.0477	PLAUR	NM_002659
TAGLN	1.14	0.0739	TAGLN	NM_003186
COL1A2	1.14	0.0818	COL1A2	NM_000089
S100A2	1.14	0.0045	S100A2	NM_005978
AKT3	1.14	0.0949	AKT3	NM_005465
SEMA3B	1.13	0.0467	SEMA3B	NM_004636
BRK	1.13	0.0476	PTK6	NM_005975
OSM	1.13	0.0344	OSM	NM_020530
SFRP2	1.12	0.0279	SFRP2	NM_003013
MRP3	1.12	0.0946	ABCC3	NM_003786
EGLN3	1.12	0.0452	EGLN3	NM_022073
SIAT7B	1.12	0.0603	ST6GALNAC2	NM_006456
OPN, osteopontin	1.12	0.0082	SPP1	NM_000582
S100P	1.12	0.0313	S100P	NM_005980
AKAP12	1.12	0.0865	AKAP12	NM_005100
MMP7	1.11	0.0909	MMP7	NM_002423
FABP4	1.11	0.0214	FABP4	NM_001442
CRYAB	1.11	0.0960	CRYAB	NM_001885
SFRP4	1.10	0.0625	SFRP4	NM_003014
EFNA3	1.10	0.0707	EFNA3	NM_004952
GSTT1	1.09	0.0516	GSTT1	NM_000853
pS2	1.08	0.0313	TFF1	NM_003225
REG4	1.08	0.0080	REG4	NM_032044
IGFBP2	1.08	0.0846	IGFBP2	NM_000597
MUC5B	1.08	0.0387	MUC5B	XM_039877

Table 3.2B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DFS as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
HSPA8	0.72	0.0604	HSPA8	NM_006597
SLC25A3	0.73	0.0126	SLC25A3	NM_213611
E2F1	0.73	0.0019	E2F1	NM_005225
IFIT1	0.74	0.0820	IFIT1	NM_001548
PPM1D	0.74	0.0007	PPM1D	NM_003620
SKP2	0.75	0.0049	SKP2	NM_005983
RRM1	0.78	0.0224	RRM1	NM_001033
DDB1	0.79	0.0720	DDB1	NM_001923
NPM1	0.79	0.0255	NPM1	NM_002520
PRDX4	0.80	0.0570	PRDX4	NM_006406
BRCA1	0.80	0.0064	BRCA1	NM_007295
C20 orf1	0.81	0.0180	TPX2	NM_012112
Chk1	0.81	0.0148	CHEK1	NM_001274
EI24	0.81	0.0417	EI24	NM_004879
CCNE2	0.81	0.0094	CCNE2	NM_057749
HMGB1	0.82	0.0852	HMGB1	NM_002128
SURV	0.82	0.0185	BIRC5	NM_001168
KIF22	0.82	0.0264	KIF22	NM_007317
RAD54L	0.82	0.0674	RAD54L	NM_003579
c-myb (MYB official)	0.82	0.0038	MYB	NM_005375
DHFR	0.82	0.0669	DHFR	NM_000791
TNFRSF5	0.83	0.0855	CD40	NM_001250
LMNB1	0.83	0.0741	LMNB1	NM_005573
CDC20	0.85	0.0538	CDC20	NM_001255
CDCA7 v2	0.85	0.0277	CDCA7	NM_145810
FASN	0.85	0.0919	FASN	NM_004104
MCM2	0.85	0.0194	MCM2	NM_004526
ABCB1	0.85	0.0169	ABCB1	NM_000927
EIF4E	0.85	0.0902	EIF4E	NM_001968
DUT	0.86	0.0535	DUT	NM_001948
C20ORF126	0.86	0.0932	PDRG1	NM_030815
MCM6	0.86	0.0970	MCM6	NM_005915
EFP	0.87	0.0850	TRIM25	NM_005082
EPHB2	0.87	0.0314	EPHB2	NM_004442
GCLC	0.87	0.0862	GCLC	NM_001498
RCC1	0.87	0.0540	RCC1	NM_001269
AREG	0.87	0.0028	AREG	NM_001657
CMYC	0.88	0.0584	MYC	NM_002467
MYBL2	0.88	0.0567	MYBL2	NM_002466
TCF-1	0.88	0.0644	TCF1	NM_000545
EREG	0.89	0.0232	EREG	NM_001432
Cdx2	0.90	0.0354	CDX2	NM_001265
PTPRO	0.92	0.0935	PTPRO	NM_030667
cripto (TDGF1 official)	0.92	0.0950	TDGF1	NM_003212
HLA-DRB1	0.93	0.0521	HLA-DRB1	NM_002124

Table 4.2A shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio>1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DRFI as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
ALDOA	3.21	0.0189	ALDOA	NM_000034
DCK	2.60	0.0248	DCK	NM_000788
ITGB1	2.58	0.0002	ITGB1	NM_002211
COX2	2.16	0.0198	PTGS2	NM_000963
TJP1	2.10	0.0122	TJP1	NM_003257
STAT3	1.87	0.0148	STAT3	NM_003150
ANXA5	1.83	0.0043	ANXA5	NM_001154
GHI BRAF mut4	1.82	0.0024		GHI_BRAF_mut4
TIMP1	1.80	<.0001	TIMP1	NM_003254
hMLH	1.80	0.0242	MLH1	NM_000249
PADI4	1.74	0.0288	PADI4	NM_012387
rhoC	1.74	0.0093	RHOC	NM_175744
CYP3A4	1.73	0.0219	CYP3A4	NM_017460
WWOX	1.72	0.0467	WWOX	NM_016373
ANXA2	1.70	0.0081	ANXA2	NM_004039
LILRB3	1.70	0.0295	LILRB3	NM_006864
VIM	1.66	0.0015	VIM	NM_003380
FUS	1.65	0.0432	FUS	NM_004960
KCNH2 iso a/b	1.64	0.0111	KCNH2	NM_000238
RhoB	1.63	0.0019	RHOB	NM_004040
CRIP2	1.62	0.0455	CRIP2	NM_001312
AKT3	1.60	0.0004	AKT3	NM_005465
RBX1	1.60	0.0195	RBX1	NM_014248
HB-EGF	1.59	0.0032	HBEGF	NM_001945
NRP2	1.55	0.0007	NRP2	NM_003872
MSH3	1.55	0.0353	MSH3	NM_002439
PI3K	1.54	0.0651	PIK3C2B	NM_002646
BGN	1.54	0.0009	BGN	NM_001711
RAB6C	1.54	0.0210	RAB6C	NM_032144
CTSB	1.53	0.0415	CTSB	NM_001908
DLC1	1.53	0.0047	DLC1	NM_006094

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Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
p21	1.53	0.0085	CDKN1A	NM_000389
CCNE2 variant 1	1.52	0.0647	CCNE2	NM_057749
CALD1	1.51	0.0069	CALD1	NM_004342
SBA2	1.51	0.0202	WSB2	NM_018639
SIR2	1.51	0.0028	SIRT1	NM_012238
ITGA5	1.50	0.0006	ITGA5	NM_002205
RAP1GDS1	1.50	0.0317	RAP1GDS1	NM_021159
CTHRC1	1.46	0.0010	CTHRC1	NM_138455
STC1	1.46	0.0083	STC1	NM_003155
KLF6	1.46	0.0362	KLF6	NM_001300
CDC42BPA	1.45	0.0187	CDC42BPA	NM_003607
CEBPB	1.45	0.0605	CEBPB	NM_005194
LAMC2	1.45	0.0031	LAMC2	NM_005562
TGFBR1	1.45	0.0824	TGFBR1	NM_004612
TLN1	1.45	0.0730	TLN1	NM_006289
CDC42	1.44	0.0387	CDC42	NM_001791
FYN	1.43	0.0070	FYN	NM_002037
IGFBP7	1.43	0.0283	IGFBP7	NM_001553
ARG	1.43	0.0119	ABL2	NM_005158
HIF1A	1.42	0.0397	HIF1A	NM_001530
FST	1.42	0.0460	FST	NM_006350
S100A1	1.42	0.0473	S100A1	NM_006271
FAP	1.42	0.0023	FAP	NM_004460
DUSP1	1.42	0.0014	DUSP1	NM_004417
EPAS1	1.41	0.0494	EPAS1	NM_001430
Grb10	1.41	0.0027	GRB10	NM_005311
VEGFC	1.41	0.0894	VEGFC	NM_005429
INHBB	1.41	0.0710	INHBB	NM_002193
GADD45B	1.40	0.0023	GADD45B	NM_015675
UBC	1.40	0.0368	UBC	NM_021009
GJA1	1.40	0.0053	GJA1	NM_000165
COL1A2	1.40	0.0086	COL1A2	NM_000089
RBM5	1.40	0.0423	RBM5	NM_005778
ROCK1	1.39	0.0604	ROCK1	NM_005406
CTGF	1.39	0.0081	CTGF	NM_001901
FLT4	1.39	0.0978	FLT4	NM_002020
PDGFC	1.39	0.0052	PDGFC	NM_016205
INHBA	1.39	0.0058	INHBA	NM_002192
LOXL2	1.38	0.0209	LOXL2	NM_002318
THBS1	1.37	0.0090	THBS1	NM_003246
ITGAV	1.37	0.0298	ITGAV	NM_002210
NCAM1	1.36	0.0714	NCAM1	NM_000615
PTHR1	1.35	0.0410	PTHR1	NM_000316
TIMP2	1.35	0.0446	TIMP2	NM_003255
LOX	1.35	0.0041	LOX	NM_002317
SPARC	1.35	0.0292	SPARC	NM_003118
TAGLN	1.34	0.0222	TAGLN	NM_003186
CYR61	1.34	0.0086	CYR61	NM_001554
RANBP9	1.34	0.0553	RANBP9	NM_005493
GADD45	1.34	0.0604	GADD45A	NM_001924
S100A4	1.34	0.0141	S100A4	NM_002961
SNAI2	1.33	0.0263	SNAI2	NM_003068
EGR1	1.33	0.0174	EGR1	NM_001964
CDH11	1.33	0.0355	CDH11	NM_001797
SI	1.33	0.0967	SI	NM_001041
PTK2	1.33	0.0911	PTK2	NM_005607
MCP1	1.32	0.0215	CCL2	NM_002982
PCAF	1.32	0.0463	PCAF	NM_003884
c-abl	1.32	0.0868	ABL1	NM_005157
TIMP3	1.32	0.0455	TIMP3	NM_000362
ANGPT2	1.31	0.0711	ANGPT2	NM_001147
NOTCH2	1.30	0.0645	NOTCH2	NM_024408
GBP2	1.30	0.0218	GBP2	NM_004120
PAI1	1.30	0.0022	SERPINE1	NM_000602
CXCR4	1.30	0.0341	CXCR4	NM_003467
BCAS1	1.30	0.0060	BCAS1	NM_003657
COL1A1	1.29	0.0349	COL1A1	NM_000088
PIM1	1.29	0.0507	PIM1	NM_002648
PDGFB	1.29	0.0288	PDGFB	NM_002608
Bcl2	1.29	0.0270	BCL2	NM_000633
SLPI	1.29	0.0222	SLPI	NM_003064
IGFBP5	1.29	0.0676	IGFBP5	NM_000599
ANXA1	1.29	0.0690	ANXA1	NM_000700
FGFR1	1.28	0.0790	FGFR1	NM_023109
CAPG	1.28	0.0987	CAPG	NM_001747
PRKCA	1.28	0.0548	PRKCA	NM_002737
EPHA2	1.28	0.0339	EPHA2	NM_004431
AKAP12	1.28	0.0215	AKAP12	NM_005100
FOS	1.28	0.0219	FOS	NM_005252
CXCL12	1.27	0.0169	CXCL12	NM_000609
GCNT1	1.27	0.0875	GCNT1	NM_001490
IGFBP3	1.27	0.0499	IGFBP3	NM_000598
DPYD	1.27	0.0259	DPYD	NM_000110
CD68	1.27	0.0752	CD68	NM_001251
EFNA1	1.27	0.0890	EFNA1	NM_004428
ABCC5	1.26	0.0536	ABCC5	NM_005688
TUBB	1.26	0.0635	TUBB2	NM_001069
PDGFA	1.26	0.0676		NM_002607
DAPK1	1.26	0.0701	DAPK1	NM_004938
SFRP2	1.25	0.0109	SFRP2	NM_003013
ID3	1.25	0.0744	ID3	NM_002167
CTSL	1.25	0.0679	CTSL	NM_001912
LAMA3	1.25	0.0299	LAMA3	NM_000227
KRT19	1.25	0.0982	KRT19	NM_002276
S100A8	1.25	0.0228	S100A8	NM_002964
IL6	1.25	0.0933	IL6	NM_000600
MRP3	1.25	0.0538	ABCC3	NM_003786
FES	1.25	0.0694	FES	NM_002005
AP-1 (JUN official)	1.25	0.0974	JUN	NM_002228
WISP1	1.24	0.0897	WISP1	NM_003882
SFRP4	1.24	0.0250	SFRP4	NM_003014
TGFBI	1.24	0.0692	TGFBI	NM_000358
Maspin	1.24	0.0152	SERPINB5	NM_002639
HOXB7	1.23	0.0541	HOXB7	NM_004502
P14ARF	1.23	0.0944		S78535
HSPA1A	1.23	0.0259	HSPA1A	NM_005345
EGR3	1.22	0.0312	EGR3	NM_004430
CRYAB	1.22	0.0483	CRYAB	NM_001885
ALDH1A1	1.22	0.0372	ALDH1A1	NM_000689
TGFB3	1.22	0.0673	TGFB3	NM_003239
KLK6	1.21	0.0288	KLK6	NM_002774
ANTXR1	1.21	0.0942	ANTXR1	NM_032208
FZD6	1.20	0.0479	FZD6	NM_003506
ILT-2	1.20	0.0930	LILRB1	NM_006669
S100A2	1.20	0.0116	S100A2	NM_005978
MMP7	1.18	0.0987	MMP7	NM_002423
FABP4	1.17	0.0371	FABP4	NM_001442
OPN, osteopontin	1.17	0.0301	SPP1	NM_000582
KLK10	1.16	0.0581	KLK10	NM_002776
pS2	1.15	0.0186	TEF1	NM_003225
REG4	1.14	0.0053	REG4	NM_032044
MUC2	1.09	0.0429	MUC2	NM_002457

Table 4.2B shows associations between clinical outcome and gene expression for those genes which demonstrated a Hazard Ratio<1.0 and for which p<0.1. Univariate Cox Proportional Hazards Regression analysis was applied in combined Stage II (Duke's B) and Stage III (Duke's C) patients using DRFI as the metric for clinical outcome.

Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
HSPA8	0.48	0.0114	HSPA8	NM_006597
RPS13	0.64	0.0082	RPS13	NM_001017
NDUFS3	0.66	0.0096	NDUFS3	NM_004551
ST14	0.66	0.0132	ST14	NM_021978
LMNB1	0.66	0.0135	LMNB1	NM_005573
TMSB4X	0.67	0.0039	TMSB4X	NM_021109
DHFR	0.68	0.0260	DHFR	NM_000791
BRCA1	0.68	0.0029	BRCA1	NM_007295
SKP2	0.68	0.0151	SKP2	NM_005983
SLC25A3	0.69	0.0265	SLC25A3	NM_213611
CDC20	0.69	0.0048	CDC20	NM_001255
RPLPO	0.70	0.0320	RPLP0	NM_001002
TCF-1	0.70	0.0013	TCF1	NM_000545

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Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
RRM1	0.71	0.0598	RRM1	NM_001033
ATP5A1	0.71	0.0827	ATP5A1	NM_004046
NME1	0.73	0.0378	NME1	NM_000269
CKS2	0.74	0.0537	CKS2	NM_001827
EI24	0.74	0.0639	EI24	NM_004879
C20 orf1	0.74	0.0435	TPX2	NM_012112
SDC1	0.74	0.0930	SDC1	NM_002997
CSEL1	0.75	0.0443	CSE1L	NM_001316
ABCC6	0.76	0.0416	ABCC6	NM_001171
MCM2	0.76	0.0136	MCM2	NM_004526
NFKBp65	0.77	0.0672	RELA	NM_021975
EPHB2	0.77	0.0133	EPHB2	NM_004442
FASN	0.78	0.0980	FASN	NM_004104
AURKB	0.78	0.0528	AURKB	NM_004217
VDR	0.79	0.0832	VDR	NM_000376
UMPS	0.80	0.0721	UMPS	NM_000373
UBE2C	0.81	0.0860	UBE2C	NM_007019
CMYC	0.82	0.0742	MYC	NM_002467

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Gene	Hazard Ratio	P Value	Official Symbol	Accession Number
MYBL2	0.83	0.0780	MYBL2	NM_002466
Cdx2	0.84	0.0392	CDX2	NM_001265
MX1	0.85	0.0786	MX1	NM_002462
EREG	0.85	0.0638	EREG	NM_001432
AREG	0.85	0.0295	AREG	NM_001657

Table 5.2A shows associations between gene expression and RFI, controlling for particular demographic and clinical characteristics of patients included in the analysis. All genes are listed whose expression correlates with RFI (p<0.1) and which demonstrated a Hazard Ratio>1 in a multivariate analysis including the following variables: tumor location, year of surgery, tumor grade, treatment protocol (C-01 or C-02), BCG treatment (yes or no), and classification of patients according to lymph node status as follows: 0 positive nodes and <12 nodes examined, 0 positive nodes and ≧12 nodes examined, 1-3 positive nodes, and ≧4 positive nodes.

Gene	Hazard Ratio	LR Chi-Square	DF	P Value	Official Symbol	Accession Number
RARB	2.02	3.42	1	0.0644	RARB	NM_016152
COX2	1.69	3.13	1	0.0768	PTGS2	NM_000963
RhoC	1.60	8.71	1	0.0032	RHOC	NM_175744
CYP3A4	1.57	5.15	1	0.0233	CYP3A4	NM_017460
RhoB	1.54	12.40	1	0.0004	RHOB	NM_004040
ANXA2	1.54	7.01	1	0.0081	ANXA2	NM_004039
ITGB1	1.54	5.54	1	0.0186	ITGB1	NM_002211
NTN1	1.53	3.63	1	0.0568	NTN1	NM_004822
KRAS2	1.51	4.83	1	0.0279	KRAS	NM_004985
IGFBP7	1.44	8.53	1	0.0035	IGFBP7	NM_001553
TIMP1	1.43	9.03	1	0.0027	TIMP1	NM_003254
WWOX	1.43	2.73	1	0.0988	WWOX	NM_016373
CYP1B1	1.39	3.69	1	0.0548	CYP1B1	NM_000104
KCNH2 iso a/b	1.38	3.23	1	0.0723	KCNH2	NM_000238
STC1	1.37	6.55	1	0.0105	STC1	NM_003155
ITGAV	1.37	9.37	1	0.0022	ITGAV	NM_002210
VEGFC	1.37	3.62	1	0.0571	VEGFC	NM_005429
G-Catenin	1.36	4.78	1	0.0287	JUP	NM_002230
S100A1	1.34	4.12	1	0.0423	S100A1	NM_006271
GADD45B	1.34	9.63	1	0.0019	GADD45B	NM_015675
NCAM1	1.33	3.00	1	0.0832	NCAM1	NM_000615
CALD1	1.33	6.05	1	0.0139	CALD1	NM_004342
FST	1.33	4.24	1	0.0396	FST	NM_006350
INHBA	1.33	9.68	1	0.0019	INHBA	NM_002192
BGN	1.33	7.27	1	0.0070	BGN	NM_001711
Claudin 4	1.33	7.13	1	0.0076	CLDN4	NM_001305
CEBPB	1.33	2.96	1	0.0851	CEBPB	NM_005194
LAMC2	1.32	8.62	1	0.0033	LAMC2	NM_005562
SPINT2	1.32	3.14	1	0.0762	SPINT2	NM_021102
AKT3	1.32	7.54	1	0.0060	AKT3	NM_005465
TIMP3	1.32	6.33	1	0.0119	TIMP3	NM_000362
MAPK14	1.31	2.75	1	0.0972	MAPK14	NM_139012
HB-EGF	1.31	4.74	1	0.0294	HBEGF	NM_001945
DUSP1	1.30	11.34	1	0.0008	DUSP1	NM_004417
EFNA1	1.30	5.87	1	0.0154	EFNA1	NM_004428
PTK2	1.29	3.60	1	0.0576	PTK2	NM_005607
DLC1	1.29	5.19	1	0.0227	DLC1	NM_006094
EPAS1	1.28	3.30	1	0.0693	EPAS1	NM_001430
THBS1	1.28	7.51	1	0.0061	THBS1	NM_003246
TIMP2	1.28	4.20	1	0.0404	TIMP2	NM_003255
TGFBI	1.27	6.68	1	0.0098	TGFBI	NM_000358
DKK1	1.27	3.05	1	0.0806	DKK1	NM_012242
SPARC	1.26	4.37	1	0.0366	SPARC	NM_003118
PDGFC	1.26	6.74	1	0.0094	PDGFC	NM_016205
RAB6C	1.26	3.27	1	0.0704	RAB6C	NM_032144
LOXL2	1.26	4.48	1	0.0343	LOXL2	NM_002318
CD68	1.25	4.68	1	0.0305	CD68	NM_001251
LOX	1.25	7.16	1	0.0075	LOX	NM_002317
CDC42BPA	1.25	3.35	1	0.0671	CDC42BPA	NM_003607

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Gene	Hazard Ratio	LR Chi-Square	DF	P Value	Official Symbol	Accession Number
TAGLN	1.25	4.83	1	0.0279	TAGLN	NM_003186
CTHRC1	1.25	5.96	1	0.0146	CTHRC1	NM_138455
PDGFA	1.25	4.63	1	0.0314		NM_002607
TMEPAI	1.24	5.63	1	0.0176	TMEPAI	NM_020182
RAB32	1.24	4.48	1	0.0343	RAB32	NM_006834
HSPA1A	1.24	8.19	1	0.0042	HSPA1A	NM_005345
VIM	1.24	2.97	1	0.0848	VIM	NM_003380
IGFBP5	1.23	3.69	1	0.0549	IGFBP5	NM_000599
EGR1	1.23	5.12	1	0.0236	EGR1	NM_001964
ANGPT2	1.23	2.96	1	0.0852	ANGPT2	NM_001147
NDRG1	1.22	2.91	1	0.0879	NDRG1	NM_006096
VEGF_altsplice1	1.22	4.08	1	0.0433		AF486837
SLPI	1.22	4.94	1	0.0262	SLPI	NM_003064
FOS	1.22	5.67	1	0.0172	FOS	NM_005252
VEGF	1.22	2.80	1	0.0942	VEGF	NM_003376
ADAMTS12	1.22	4.40	1	0.0359	ADAMTS12	NM_030955
Maspin	1.22	7.60	1	0.0058	SERPINB5	NM_002639
CGB	1.22	3.25	1	0.0713	CGB	NM_000737
CYR61	1.21	5.22	1	0.0224	CYR61	NM_001554
GJB2	1.21	3.77	1	0.0522	GJB2	NM_004004
IGFBP3	1.21	4.24	1	0.0396	IGFBP3	NM_000598
PRKCA	1.21	3.81	1	0.0508	PRKCA	NM_002737
S100P	1.21	6.98	1	0.0082	S100P	NM_005980
NRP2	1.21	3.25	1	0.0714	NRP2	NM_003872
EFNB2	1.21	3.00	1	0.0834	EFNB2	NM_004093
COL1A2	1.21	3.59	1	0.0581	COL1A2	NM_000089
VEGFB	1.20	2.80	1	0.0942	VEGFB	NM_003377
HOXB7	1.20	4.37	1	0.0367	HOXB7	NM_004502
Grb10	1.20	3.91	1	0.0480	GRB10	NM_005311
FAP	1.20	4.12	1	0.0425	FAP	NM_004460
GJA1	1.20	4.80	1	0.0285	GJA1	NM_000165
CTGF	1.19	3.38	1	0.0660	CTGF	NM_001901
NR4A1	1.18	5.13	1	0.0235	NR4A1	NM_002135
COL1A1	1.18	2.77	1	0.0961	COL1A1	NM_000088
ABCC5	1.17	2.80	1	0.0945	ABCC5	NM_005688
EMP1	1.17	3.06	1	0.0804	EMP1	NM_001423
SFRP2	1.17	4.89	1	0.0270	SFRP2	NM_003013
SLC2A1	1.17	3.52	1	0.0606	SLC2A1	NM_006516
F3	1.17	3.10	1	0.0783	F3	NM_001993
S100A4	1.17	2.87	1	0.0900	S100A4	NM_002961
BRK	1.17	2.81	1	0.0935	PTK6	NM_005975
CRYAB	1.17	3.77	1	0.0523	CRYAB	NM_001885
MDK	1.16	3.84	1	0.0500	MDK	NM_002391
OPN, osteopontin	1.16	6.07	1	0.0138	SPP1	NM_000582
SFRP4	1.16	4.09	1	0.0432	SFRP4	NM_003014
SIAT4A	1.16	2.76	1	0.0969	ST3GAL1	NM_003033
LAMA3	1.16	3.23	1	0.0725	LAMA3	NM_000227
AKAP12	1.15	2.74	1	0.0976	AKAP12	NM_005100
KLK10	1.15	5.23	1	0.0221	KLK10	NM_002776
EGR3	1.14	3.16	1	0.0755	EGR3	NM_004430
PAI1	1.13	3.39	1	0.0655	SERPINE1	NM_000602
CEACAM6	1.13	2.98	1	0.0845	CEACAM6	NM_002483
KLK6	1.13	3.74	1	0.0532	KLK6	NM_002774
Nkd-1	1.11	3.34	1	0.0674	NKD1	NM_033119
IGFBP2	1.11	3.15	1	0.0758	IGFBP2	NM_000597
REG4	1.08	3.51	1	0.0610	REG4	NM_032044

Table 5.2B shows associations between gene expression and RFI, controlling for particular demographic and clinical characteristics of patients included in the analysis. All genes are listed whose expression correlates with RFI ($p<0.1$) and which demonstrated a Hazard Ratio<1 in a multivariate analysis including the following variables: tumor location, year of surgery, tumor grade, treatment protocol (C-01 or C-02), BCG treatment (yes or no), and classification of patients according to lymph node status as follows: 0 positive nodes and <12 nodes examined, 0 positive nodes and ≧12 nodes examined, 1-3 positive nodes, and ≧4 positive nodes.

Gene	Hazard Ratio	LR Chi-Square	DF	P Value	Official Symbol	Accession Number
Fasl	0.43	5.57	1	0.0183	FASLG	NM_000639
BFGF	0.57	4.68	1	0.0306	NUDT6	NM_007083

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Gene	Hazard Ratio	LR Chi-Square	DF	P Value	Official Symbol	Accession Number
EstR1	0.57	3.22	1	0.0726	ESR1	NM_000125
IFIT1	0.60	4.30	1	0.0381	IFIT1	NM_001548
KLRK1	0.64	10.81	1	0.0010	KLRK1	NM_007360
E2F1	0.65	7.49	1	0.0062	E2F1	NM_005225
BRCA1	0.66	16.33	1	<.0001	BRCA1	NM_007295
RAD54L	0.67	6.36	1	0.0117	RAD54L	NM_003579
ATP5A1	0.67	5.50	1	0.0190	ATP5A1	NM_004046
MCM3	0.68	2.84	1	0.0922	MCM3	NM_002388
DHFR	0.68	7.44	1	0.0064	DHFR	NM_000791
HSPA8	0.68	2.96	1	0.0855	HSPA8	NM_006597
APG-1	0.71	5.86	1	0.0155	HSPA4L	NM_014278
BRCA2	0.71	4.69	1	0.0304	BRCA2	NM_000059
TRAIL	0.71	7.27	1	0.0070	TNFSF10	NM_003810
SLC25A3	0.71	5.56	1	0.0184	SLC25A3	NM_213611
PPM1D	0.72	8.02	1	0.0046	PPM1D	NM_003620
Chk1	0.73	6.61	1	0.0102	CHEK1	NM_001274
CD80	0.73	6.85	1	0.0089	CD80	NM_005191
MADH2	0.73	3.93	1	0.0476	SMAD2	NM_005901
KIF22	0.75	5.77	1	0.0163	KIF22	NM_007317
TNFRSF5	0.76	3.52	1	0.0607	CD40	NM_001250
C20 orf1	0.76	4.82	1	0.0281	TPX2	NM_012112
ENO1	0.76	2.88	1	0.0894	ENO1	NM_001428
PRKCB1	0.77	4.25	1	0.0393	PRKCB1	NM_002738
RAF1	0.77	4.17	1	0.0412	RAF1	NM_002880
RRM1	0.78	3.07	1	0.0799	RRM1	NM_001033
UBE2M	0.78	4.43	1	0.0352	UBE2M	NM_003969
SKP2	0.79	3.42	1	0.0644	SKP2	NM_005983
DUT	0.79	4.38	1	0.0364	DUT	NM_001948
EI24	0.80	2.85	1	0.0912	EI24	NM_004879
UMPS	0.80	4.96	1	0.0260	UMPS	NM_000373
EFP	0.81	3.83	1	0.0502	TRIM25	NM_005082
HRAS	0.81	3.80	1	0.0513	HRAS	NM_005343
CDC20	0.81	3.78	1	0.0519	CDC20	NM_001255
CSF1	0.82	2.86	1	0.0910	CSF1	NM_000757
CKS2	0.82	2.90	1	0.0886	CKS2	NM_001827
ABCB1	0.82	4.02	1	0.0450	ABCB1	NM_000927
CDC6	0.83	4.23	1	0.0397	CDC6	NM_001254
GBP1	0.83	4.34	1	0.0373	GBP1	NM_002053
SURV	0.83	2.91	1	0.0878	BIRC5	NM_001168
CCNE2	0.83	2.75	1	0.0975	CCNE2	NM_057749
RRM2	0.83	4.19	1	0.0407	RRM2	NM_001034
CMYC	0.84	3.34	1	0.0677	MYC	NM_002467
TCF-1	0.84	3.96	1	0.0466	TCF1	NM_000545
c-myb (MYB official)	0.84	3.72	1	0.0538	MYB	NM_005375
NOTCH1	0.85	3.39	1	0.0658	NOTCH1	NM_017617
MCM2	0.85	3.30	1	0.0693	MCM2	NM_004526
ING5	0.85	2.84	1	0.0922	ING5	NM_032329
AREG	0.88	3.72	1	0.0538	AREG	NM_001657
HLA-DRB1	0.90	3.84	1	0.0500	HLA-DRB1	NM_002124

Table 6.2 shows associations between gene expression and clinical outcome based on a nonlinear proportional hazards analysis, using a 2 degree-of-freedom natural spline. All genes are listed which demonstrated a departure from a strictly linear relationship (p<0.05) with RFI in combined Stage II (Duke's B) and Stage III (Duke's C) patients. The relationship between gene expression and RFI was not constant throughout the observed range of expression values in the study, e.g. increases in gene expression may have been related to increases in duration of RFI in one portion of the observed range and with decreases in duration of RFI in a different portion of the range.

Gene	P Value	Official Symbol	Accession Number
PTHLH	<.0001	PTHLH	NM_002820
TGFBR1	0.0011	TGFBR1	NM_004612
CDCA7 v2	0.0020	CDCA7	NM_145810
S100A4	0.0034	S100A4	NM_002961
CREBBP	0.0040	CREBBP	NM_004380
Upa	0.0040	PLAU	NM_002658
KLF5	0.0048	KLF5	NM_001730
CYP2C8	0.0070	CYP2C8	NM_000770
HES6	0.0090	HES6	NM_018645
Cad17	0.0093	CDH17	NM_004063
CEGP1	0.0100	SCUBE2	NM_020974
GHI k-ras mut3	0.0100		GHI_k-ras_mut3
AKT1	0.0104	AKT1	NM_005163
LAMB3	0.0111	LAMB3	NM_000228
CAPG	0.0120	CAPG	NM_001747
FUT6	0.0130	FUT6	NM_000150
A-Catenin	0.0141	CTNNA1	NM_001903
CAPN1	0.0167	CAPN1	NM_005186
HSPE1	0.0180	HSPE1	NM_002157

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Gene	P Value	Official Symbol	Accession Number
MADH4	0.0180	SMAD4	NM_005359
STMY3	0.0190	MMP11	NM_005940
TRAG3	0.0200	CSAG2	NM_004909
GBP1	0.0200	GBP1	NM_002053
EFNA1	0.0210	EFNA1	NM_004428
SEMA3B	0.0210	SEMA3B	NM_004636
CLTC	0.0216	CLTC	NM_004859
BRK	0.0240	PTK6	NM_005975
Fas	0.0240	FAS	NM_000043
CCNE2 variant 1	0.0243	CCNE2	NM_057749
TMEPAI	0.0246	TMEPAI	NM_020182
PTPRJ	0.0260	PTPRJ	NM_002843
SKP2	0.0261	SKP2	NM_005983
AGXT	0.0273	AGXT	NM_000030
MAP2	0.0320	MAP2	NM_031846
PFN2	0.0330	PFN2	NM_053024
ATP5E	0.0350	ATP5E	NM_006886
NRP1	0.0352	NRP1	NM_003873
MYH11	0.0360	MYH11	NM_002474
cIAP2	0.0369	BIRC3	NM_001165
INHBA	0.0370	INHBA	NM_002192
EGLN1	0.0371	EGLN1	NM_022051
GRIK1	0.0380	GRIK1	NM_000830
KDR	0.0380	KDR	NM_002253
KLK6	0.0388	KLK6	NM_002774
APOC1	0.0390	APOC1	NM_001645
EP300	0.0390	EP300	NM_001429
DET1	0.0390	DET1	NM_017996
ITGB4	0.0394	ITGB4	NM_000213
CD3z	0.0400	CD3Z	NM_000734
MAX	0.0400	MAX	NM_002382
PAI1	0.0407	SERPINE1	NM_000602
MADH7	0.0430	SMAD7	NM_005904
SIR2	0.0440	SIRT1	NM_012238
NEDD8	0.0440	NEDD8	NM_006156
EPHB2	0.0445	EPHB2	NM_004442
BTF3	0.0460	BTF3	NM_001207
CD34	0.0470	CD34	NM_001773
VEGF_altsplice2	0.0480		AF214570
Wnt-5b	0.0480	WNT5B	NM_032642
RXRA	0.0482	RXRA	NM_002957
tusc4	0.0486	TUSC4	NM_006545

Table 7.2 shows all genes exhibiting an interaction (p-value<0.1) with tumor stage. The data were modeled using a proportional hazards model of RFI with gene expression, tumor stage, and their interaction as predictors. Patients who had 0 positive nodes but <12 nodes examined were excluded from these analyses.

Gene	HR Stage II	HR Stage III	P-Value for Inter-action	Official Symbol	Accession Number
SOS1	3.35	0.81	0.0009	SOS1	NM_005633
ALCAM	2.36	0.94	0.0020	ALCAM	NM_001627
pS2	1.58	1.04	0.0040	TFF1	NM_003225
TGFB2	1.83	0.95	0.0064	TGFB2	NM_003238
TFF3	1.57	0.90	0.0066	TFF3	NM_003226
KLF6	0.35	1.34	0.0092	KLF6	NM_001300
SNRPF	0.50	1.16	0.0106	SNRPF	NM_003095
CENPA	2.41	0.94	0.0106	CENPA	NM_001809
HES6	1.69	0.86	0.0119	HES6	NM_018645
CLDN1	0.51	0.95	0.0124	CLDN1	NM_021101
FGF2	0.19	0.97	0.0125	FGF2	NM_002006
LEF	1.94	0.94	0.0141	LEF1	NM_016269
MADH2	2.70	0.74	0.0145	SMAD2	NM_005901
TP53BP1	2.31	0.91	0.0153	TP53BP1	NM_005657
CCR7	1.89	0.98	0.0182	CCR7	NM_001838
MRP3	2.26	1.08	0.0204	ABCC3	NM_003786
UPP1	0.16	1.02	0.0208	UPP1	NM_003364
PTEN	3.46	1.00	0.0216	PTEN	NM_000314
ST14	1.64	0.66	0.0223	ST14	NM_021978
FYN	2.28	1.10	0.0241	FYN	NM_002037
CD24	1.33	0.84	0.0260	CD24	NM_013230
LMYC	1.80	0.82	0.0275	RLF	NM_012421
CDC42BPA	2.82	1.12	0.0315	CDC42BPA	NM_003607
CAV1	2.11	0.95	0.0364	CAV1	NM_001753
CHFR	1.81	0.99	0.0382	CHFR	NM_018223
MGAT5	1.59	0.72	0.0383	MGAT5	NM_002410
FPGS	1.93	0.71	0.0402	FPGS	NM_004957
EMR3	2.63	0.57	0.0488	EMR3	NM_032571
SIR2	2.17	1.07	0.0538	SIRT1	NM_012238
PTK2B	1.44	0.93	0.0542	PTK2B	NM_004103
Axin 2	1.38	0.90	0.0549	AXIN2	NM_004655
TRAG3	0.46	1.12	0.0570	CSAG2	NM_004909
MMP7	0.78	1.28	0.0608	MMP7	NM_002423
PFN2	1.33	0.84	0.0610	PFN2	NM_053024
PTPRJ	2.05	1.00	0.0632	PTPRJ	NM_002843
CXCR4	1.96	1.08	0.0644	CXCR4	NM_003467
CCNA2	1.55	0.79	0.0661	CCNA2	NM_001237
MMP12	0.74	1.11	0.0685	MMP12	NM_002426
KRT8	0.64	1.27	0.0694	KRT8	NM_002273
ABCC5	2.06	1.14	0.0704	ABCC5	NM_005688
PRDX6	2.09	0.74	0.0711	PRDX6	NM_004905
WIF	1.54	0.77	0.0738	WIF1	NM_007191
cdc25A	2.48	0.94	0.0769	CDC25A	NM_001789
KLF5	1.87	1.03	0.0772	KLF5	NM_001730
LRP5	1.92	0.98	0.0783	LRP5	NM_002335
PTPD1	0.54	1.00	0.0789	PTPN21	NM_007039
RALBP1	2.20	0.91	0.0791	RALBP1	NM_006788
TP53BP2	1.82	1.05	0.0819	TP53BP2	NM_005426
STAT5B	1.57	0.86	0.0822	STAT5B	NM_012448
PPARG	1.32	0.79	0.0844	PPARG	NM_005037
HB-EGF	0.50	1.38	0.0845	HBEGF	NM_001945
RARA	1.77	0.96	0.0848	RARA	NM_000964
GCNT1	1.86	1.07	0.0883	GCNT1	NM_001490
Ki-67	1.53	0.86	0.0885	MKI67	NM_002417
EFNB2	1.76	1.05	0.0895	EFNB2	NM_004093
LGMN	0.59	1.37	0.0900	LGMN	NM_001008530
DKK1	0.68	1.51	0.0922	DKK1	NM_012242
MADH4	2.04	0.98	0.0964	SMAD4	NM_005359
BIK	1.53	0.94	0.0966	BIK	NM_001197
CD44v3	1.58	0.97	0.0996		AJ251595v3

TABLE A

Gene	Accession	Reagent	Sequence	Sequence ID Number
A-Catenin	NM_001903.1	Forward Primer	CGTTCCGATCCTCTATACTGCAT	SEQ ID NO: 1
		Probe	ATGCCTACAGCACCCTGATGTCGCA	SEQ ID NO: 2
		Reverse Primer	AGGTCCCTGTTGGCCTTATAGG	SEQ ID NO: 3

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
ABCB1	NM_000927.2	Forward Primer	AAACACCACTGGAGCATTGA	SEQ ID NO: 4
		Probe	CTCGCCAATGATGCTGCTCAAGTT	SEQ ID NO: 5
		Reverse Primer	CAAGCCTGGAACCTATAGCC	SEQ ID NO: 6
ABCC5	NM_005688.1	Forward Primer	TGCAGACTGTACCATGCTGA	SEQ ID NO: 7
		Probe	CTGCACACGGTTCTAGGCTCCG	SEQ ID NO: 8
		Reverse Primer	GGCCAGCACCATAATCCTAT	SEQ ID NO: 9
ABCC6	NM_001171.2	Forward Primer	GGATGAACCTCGACCTGC	SEQ ID NO: 10
		Probe	CCAGATAGCCTCGTCCGAGTGCTC	SEQ ID NO: 11
		Reverse Primer	GAGCTGCACCGTCTCCAG	SEQ ID NO: 12
ACP1	NM_004300.2	Forward Primer	GCTACCAAGTCCGTGCTGT	SEQ ID NO: 13
		Probe	TGATCGACAAATGTTACCCAGACACACA	SEQ ID NO: 14
		Reverse Primer	GAAAACTGCTTCTGCAATGG	SEQ ID NO: 15
ADAM10	NM_001110.1	Forward Primer	CCCATCAACTTGTGCCAGTA	SEQ ID NO: 16
		Probe	TGCCTACTCCACTGCACAGACCCT	SEQ ID NO: 17
		Reverse Primer	GGTGATGGTTCGACCACTG	SEQ ID NO: 18
ADAM17	NM_003183.3	Forward Primer	GAAGTGCCAGGAGGCGATTA	SEQ ID NO: 19
		Probe	TGCTACTTGCAAAGGCGTGTCCTACTGC	SEQ ID NO: 20
		Reverse Primer	CGGGCACTCACTGCTATTACC	SEQ ID NO: 21
ADAMTS12	NM_030955.2	Forward Primer	GGAGAAGGGTGGAGTGCAG	SEQ ID NO: 22
		Probe	CGCACAGTCAGAATCCATCTGGGT	SEQ ID NO: 23
		Reverse Primer	CAGGGTCAGGTCTCTGGATG	SEQ ID NO: 24
ADPRT	NM_001618.2	Forward Primer	TTGACAACCTGCTGGACATC	SEQ ID NO: 25
		Probe	CCCTGAGCAGACTGTAGGCCACCT	SEQ ID NO: 26
		Reverse Primer	ATGGGATCCTTGCTGCTATC	SEQ ID NO: 27
AGXT	NM_000030.1	Forward Primer	CTTTTCCCTCCAGTGGCA	SEQ ID NO: 28
		Probe	CTCCTGGAAACAGTCCACTTGGGC	SEQ ID NO: 29
		Reverse Primer	ATTTGGAAGGCACTGGGTTT	SEQ ID NO: 30
AKAP12	NM_005100.2	Forward Primer	TAGAGAGCCCCTGACAATCC	SEQ ID NO: 31
		Probe	TGGCTCTAGCTCCTGATGAAGCCTC	SEQ ID NO: 32
		Reverse Primer	GGTTGGTCTTGGAAAGAGGA	SEQ ID NO: 33
AKT1	NM_005163.1	Forward Primer	CGCTTCTATGGCGCTGAGAT	SEQ ID NO: 34
		Probe	CAGCCCTGGACTACCTGCACTCGG	SEQ ID NO: 35
		Reverse Primer	TCCCGGTACACCACGTTCTT	SEQ ID NO: 36
AKT2	NM_001626.2	Forward Primer	TCCTGCCACCCTTCAAACC	SEQ ID NO: 37
		Probe	CAGGTCACGTCCGAGGTCGACACA	SEQ ID NO: 38
		Reverse Primer	GGCGGTAAATTCATCATCGAA	SEQ ID NO: 39
AKT3	NM_005465.1	Forward Primer	TTGTCTCTGCCTTGGACTATCTACA	SEQ ID NO: 40
		Probe	TCACGGTACACAATCTTTCCGGA	SEQ ID NO: 41
		Reverse Primer	CCAGCATTAGATTCTCCAACTTGA	SEQ ID NO: 42
AL137428	AL137428.1	Forward Primer	CAAGAAGAGGCTCTACCCTGG	SEQ ID NO: 43
		Probe	ACTGGGAATTTCCAAGGCCACCTT	SEQ ID NO: 44
		Reverse Primer	AAATGAGCTCTGCGATCCTC	SEQ ID NO: 45
ALCAM	NM_001627.1	Forward Primer	GAGGAATATGGAATCCAAGGG	SEQ ID NO: 46
		Probe	CCAGTTCCTGCCGTCTGCTCTTCT	SEQ ID NO: 47
		Reverse Primer	GTGGCGGAGATCAAGAGG	SEQ ID NO: 48
ALDH1A1	NM_000689.1	Forward Primer	GAAGGAGATAAGGAGGATGTTGACA	SEQ ID NO: 49
		Probe	AGTGAAGGCCGCAAGACAGGCTTTTC	SEQ ID NO: 50
		Reverse Primer	CGCCACGGAGATCCAATC	SEQ ID NO: 51
ALDOA	NM_000034.2	Forward Primer	GCCTGTACGTGCCAGCTC	SEQ ID NO: 52
		Probe	TGCCAGAGCCTCAACTGTCTCTGC	SEQ ID NO: 53
		Reverse Primer	TCATCGGAGCTTGATCTCG	SEQ ID NO: 54
AMFR	NM_001144.2	Forward Primer	GATGGTTCAGCTCTGCAAGGA	SEQ ID NO: 55
		Probe	CGATTTGAATATCTTTCCTTCTCGCCCACC	SEQ ID NO: 56
		Reverse Primer	TCGACCGTGGCTGCTCAT	SEQ ID NO: 57
ANGPT2	NM_001147.1	Forward Primer	CCGTGAAAGCTGCTCTGTAA	SEQ ID NO: 58
		Probe	AAGCTGACACAGCCCTCCCAAGTG	SEQ ID NO: 59
		Reverse Primer	TTGCAGTGGGAAGAACAGTC	SEQ ID NO: 60

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
ANTXR1	NM_032208.1	Forward Primer	CTCCAGGTGTACCTCCAACC	SEQ ID NO: 61
		Probe	AGCCTTCTCCCACAGCTGCCTACA	SEQ ID NO: 62
		Reverse Primer	GAGAAGGCTGGGAGACTCTG	SEQ ID NO: 63
ANXA1	NM_000700.1	Forward Primer	GCCCCTATCCTACCTTCAATCC	SEQ ID NO: 64
		Probe	TCCTCGGATGTCGCTGCCT	SEQ ID NO: 65
		Reverse Primer	CCTTTAACCATTATGGCCTTATGC	SEQ ID NO: 66
ANXA2	NM_004039.1	Forward Primer	CAAGACACTAAGGGCGACTACCA	SEQ ID NO: 67
		Probe	CCACCACACAGGTACAGCAGCGCT	SEQ ID NO: 68
		Reverse Primer	CGTGTCGGGCTTCAGTCAT	SEQ ID NO: 69
ANXA5	NM_001154.2	Forward Primer	GCTCAAGCCTGGAAGATGAC	SEQ ID NO: 70
		Probe	AGTACCCTGAAGTGTCCCCCACCA	SEQ ID NO: 71
		Reverse Primer	AGAACCACCAACATCCGCT	SEQ ID NO: 72
AP-1 (JUN official)	NM_002228.2	Forward Primer	GACTGCAAAGATGGAAACGA	SEQ ID NO: 73
		Probe	CTATGACGATGCCCTCAACGCCTC	SEQ ID NO: 74
		Reverse Primer	TAGCCATAAGGTCCGCTCTC	SEQ ID NO: 75
APC	NM_000038.1	Forward Primer	GGACAGCAGGAATGTGTTTC	SEQ ID NO: 76
		Probe	CATTGGCTCCCCGTGACCTGTA	SEQ ID NO: 77
		Reverse Primer	ACCCACTCGATTTGTTTCTG	SEQ ID NO: 78
APEX-1	NM_001641.2	Forward Primer	GATGAAGCCTTTCGCAAGTT	SEQ ID NO: 79
		Probe	CTTTCGGGAAGCCAGGCCCTT	SEQ ID NO: 80
		Reverse Primer	AGGTCTCCACACAGCACAAG	SEQ ID NO: 81
APG-1	NM_014278.2	Forward Primer	ACCCCGGCCTGTATATCAT	SEQ ID NO: 82
		Probe	CCAATGGCTCGAGTTCTTGATCCC	SEQ ID NO: 83
		Reverse Primer	CTATCTGGCTCTTTGCTGCAT	SEQ ID NO: 84
APN (ANPEP official)	NM_001150.1	Forward Primer	CCACCTTGGACCAAAGTAAAGC	SEQ ID NO: 85
		Probe	CTCCCCAACACGCTGAAACCCG	SEQ ID NO: 86
		Reverse Primer	TCTCAGCGTCACCTGGTAGGA	SEQ ID NO: 87
APOC1	NM_001645.3	Forward Primer	GGAAACACACTGGAGGACAAG	SEQ ID NO: 88
		Probe	TCATCAGCCGCATCAAACAGAGTG	SEQ ID NO: 89
		Reverse Primer	CGCATCTTGGCAGAAAGTT	SEQ ID NO: 90
AREG	NM_001657.1	Forward Primer	TGTGAGTGAAATGCCTTCTAGTAGTGA	SEQ ID NO: 91
		Probe	CCGTCCTCGGGAGCCGACTATGA	SEQ ID NO: 92
		Reverse Primer	TTGTGGTTCGTTATCATACTCTTCTGA	SEQ ID NO: 93
ARG	NM_005158.2	Forward Primer	CGCAGTGCAGCTGAGTATCTG	SEQ ID NO: 94
		Probe	TCGCACCAGGAAGCTGCCATTGA	SEQ ID NO: 95
		Reverse Primer	TGCCCAGGGCTACTCTCACTT	SEQ ID NO: 96
ARHF	NM_019034.2	Forward Primer	ACTGGCCCACTTAGTCCTCA	SEQ ID NO: 97
		Probe	CTCCCAACCTGCTGTCCCTCAAG	SEQ ID NO: 98
		Reverse Primer	CTGAACTCCACAGGCTGGTA	SEQ ID NO: 99
ATOH1	NM_005172.1	Forward Primer	GCAGCCACCTGCAACTTT	SEQ ID NO: 100
		Probe	CAGGCGAGAGAGCATCCCGTCTAC	SEQ ID NO: 101
		Reverse Primer	TCCAGGAGGGACAGCTCA	SEQ ID NO: 102
ATP5A1	NM_004046.3	Forward Primer	GATGCTGCCACTCAACAACT	SEQ ID NO: 103
		Probe	AGTTAGACGCACGCCACGACTCAA	SEQ ID NO: 104
		Reverse Primer	TGTCCTTGCTTCAGCAACTC	SEQ ID NO: 105
ATP5E	NM_006886.2	Forward Primer	CCGCTTTCGCTACAGCAT	SEQ ID NO: 106
		Probe	TCCAGCCTGTCTCCAGTAGGCCAC	SEQ ID NO: 107
		Reverse Primer	TGGGAGTATCGGATGTAGCTG	SEQ ID NO: 108
AURKB	NM_004217.1	Forward Primer	AGCTGCAGAAGAGCTGCACAT	SEQ ID NO: 109
		Probe	TGACGAGCAGCGAACAGCCACG	SEQ ID NO: 110
		Reverse Primer	GCATCTGCCAACTCCTCCAT	SEQ ID NO: 111
Axin 2	NM_004655.2	Forward Primer	GGCTATGTCTTTGCACCAGC	SEQ ID NO: 112
		Probe	ACCAGCGCCAACGACAGTGAGATA	SEQ ID NO: 113
		Reverse Primer	ATCCGTCAGCGCATCACT	SEQ ID NO: 114
axin1	NM_003502.2	Forward Primer	CCGTGTGACAGCATCGTT	SEQ ID NO: 115
		Probe	CGTACTACTTCTGCGGGGAACCCA	SEQ ID NO: 116
		Reverse Primer	CTCACCAGGGTGCGGTAG	SEQ ID NO: 117

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
B-Catenin	NM_001904.1	Forward Primer	GGCTCTTGTGCGTACTGTCCTT	SEQ ID NO: 118
		Probe	AGGCTCAGTGATGTCTTCCCTGTCACCAG	SEQ ID NO: 119
		Reverse Primer	TCAGATGACGAAGAGCACAGATG	SEQ ID NO: 120
BAD	NM_032989.1	Forward Primer	GGGTCAGGTGCCTCGAGAT	SEQ ID NO: 121
		Probe	TGGGCCCAGAGCATGTTCCAGATC	SEQ ID NO: 122
		Reverse Primer	CTGCTCACTCGGCTCAAACTC	SEQ ID NO: 123
BAG1	NM_004323.2	Forward Primer	CGTTGTCAGCACTTGGAATACAA	SEQ ID NO: 124
		Probe	CCCAATTAACATGACCCGGCAACCAT	SEQ ID NO: 125
		Reverse Primer	GTTCAACCTCTTCCTGTGGACTGT	SEQ ID NO: 126
BAG2	NM_004282.2	Forward Primer	CTAGGGGCAAAAAGCATGA	SEQ ID NO: 127
		Probe	TTCCATGCCAGACAGGAAAAAGCA	SEQ ID NO: 128
		Reverse Primer	CTAAATGCCCAAGGTGACTG	SEQ ID NO: 129
BAG3	NM_004281.2	Forward Primer	GAAAGTAAGCCAGGCCCAGTT	SEQ ID NO: 130
		Probe	CAGAACTCCCTCCTGGACACATCCCAA	SEQ ID NO: 131
		Reverse Primer	ACCTCTTTGCGGATCACTTGA	SEQ ID NO: 132
Bak	NM_001188.1	Forward Primer	CCATTCCCACCATTCTACCT	SEQ ID NO: 133
		Probe	ACACCCCAGACGTCCTGGCCT	SEQ ID NO: 134
		Reverse Primer	GGGAACATAGACCCACCAAT	SEQ ID NO: 135
Bax	NM_004324.1	Forward Primer	CCGCCGTGGACACAGACT	SEQ ID NO: 136
		Probe	TGCCACTCGGAAAAAGACCTCTCGG	SEQ ID NO: 137
		Reverse Primer	TTGCCGTCAGAAAACATGTCA	SEQ ID NO: 138
BBC3	NM_014417.1	Forward Primer	CCTGGAGGGTCCTGTACAAT	SEQ ID NO: 139
		Probe	CATCATGGGACTCCTGCCCTTACC	SEQ ID NO: 140
		Reverse Primer	CTAATTGGGCTCCATCTCG	SEQ ID NO: 141
BCAS1	NM_003657.1	Forward Primer	CCCCGAGACAACGGAGATAA	SEQ ID NO: 142
		Probe	CTTTCCGTTGGCATCCGCAACAG	SEQ ID NO: 143
		Reverse Primer	CTCGGGTTTGGCCTCTTTC	SEQ ID NO: 144
Bcl2	NM_000633.1	Forward Primer	CAGATGGACCTAGTACCCACTGAGA	SEQ ID NO: 145
		Probe	TTCCACGCCGAAGGACAGCGAT	SEQ ID NO: 146
		Reverse Primer	CCTATGATTTAAGGGCATTTTTCC	SEQ ID NO: 147
BCL2L10	NM_020396.2	Forward Primer	GCTGGGATGGCTTTTGTCA	SEQ ID NO: 148
		Probe	TCTTCAGGACCCCCTTTCCACTGGC	SEQ ID NO: 149
		Reverse Primer	GCCTGGACCAGCTGTTTTCTC	SEQ ID NO: 150
BCL2L11	NM_138621.1	Forward Primer	AATTACCAAGCAGCCGAAGA	SEQ ID NO: 151
		Probe	CCACCCACGAATGGTTATCTTACGACTG	SEQ ID NO: 152
		Reverse Primer	CAGGCGGACAATGTAACGTA	SEQ ID NO: 153
BCL2L12	NM_138639.1	Forward Primer	AACCCACCCCTGTCTTGG	SEQ ID NO: 154
		Probe	TCCGGGTAGCTCTCAAACTCGAGG	SEQ ID NO: 155
		Reverse Primer	CTCAGCTGACGGGAAAGG	SEQ ID NO: 156
Bclx	NM_001191.1	Forward Primer	CTTTTGTGGAACTCTATGGGAACA	SEQ ID NO: 157
		Probe	TTCGGCTCTCGGCTGCTGCA	SEQ ID NO: 158
		Reverse Primer	CAGCGGTTGAAGCGTTCCT	SEQ ID NO: 159
BCRP	NM_004827.1	Forward Primer	TGTACTGGCGAAGAATATTTGGTAAA	SEQ ID NO: 160
		Probe	CAGGGCATCGATCTCTCACCCTGG	SEQ ID NO: 161
		Reverse Primer	GCCACGTGATTCTTCCACAA	SEQ ID NO: 162
BFGF	NM_007083.1	Forward Primer	CCAGGAAGAATGCTTAAGATGTGA	SEQ ID NO: 163
		Probe	TTCGCCAGGTCATTGAGATCCATCCA	SEQ ID NO: 164
		Reverse Primer	TGGTGATGGGAGTTGTATTTTCAG	SEQ ID NO: 165
BGN	NM_001711.3	Forward Primer	GAGCTCCGCAAGGATGAC	SEQ ID NO: 166
		Probe	CAAGGGTCTCCAGCACCTCTACGC	SEQ ID NO: 167
		Reverse Primer	CTTGTTGTTCACCAGGACGA	SEQ ID NO: 168
BID	NM_001196.2	Forward Primer	GGACTGTGAGGTCAACAACG	SEQ ID NO: 169
		Probe	TGTGATGCACTCATCCCTGAGGCT	SEQ ID NO: 170
		Reverse Primer	GGAAGCCAAACACCAGTAGG	SEQ ID NO: 171
BIK	NM_001197.3	Forward Primer	ATTCCTATGGCTCTGCAATTGTC	SEQ ID NO: 172
		Probe	CCGGTTAACTGTGGCCTGTGCCC	SEQ ID NO: 173
		Reverse Primer	GGCAGGAGTGAATGGCTCTTC	SEQ ID NO: 174

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
BIN1	NM_004305.1	Forward Primer	CCTGCAAAAGGGAACAAGAG	SEQ ID NO: 175
		Probe	CTTCGCCTCCAGATGGCTCCC	SEQ ID NO: 176
		Reverse Primer	CGTGGTTGACTCTGATCTCG	SEQ ID NO: 177
BLMH	NM_000386.2	Forward Primer	GGTTGCTGCCTCCATCAAAG	SEQ ID NO: 178
		Probe	ACATCACAGCCAAACCACACAGCCTCT	SEQ ID NO: 179
		Reverse Primer	CCAGCTTGCTATTGAAGTGTTTTC	SEQ ID NO: 180
BMP2	NM_001200.1	Forward Primer	ATGTGGACGCTCTTTCAATG	SEQ ID NO: 181
		Probe	ACCGCAGTCCGTCTAAGAAGCACG	SEQ ID NO: 182
		Reverse Primer	ACCATGGTCGACCTTTAGGA	SEQ ID NO: 183
BMP4	NM_001202.2	Forward Primer	GGGCTAGCCATTGAGGTG	SEQ ID NO: 184
		Probe	CTCACCTCCATCAGACTCGGACCC	SEQ ID NO: 185
		Reverse Primer	GCTAATCCTGACATGCTGGC	SEQ ID NO: 186
BMP7	NM_001719.1	Forward Primer	TCGTGGAACATGACAAGGAATT	SEQ ID NO: 187
		Probe	TTCCACCCACGCTACCACCATCG	SEQ ID NO: 188
		Reverse Primer	TGGAAAGATCAAACCGGAACTC	SEQ ID NO: 189
BMPR1A	NM_004329.2	Forward Primer	TTGGTTCAGCGAACTATTGC	SEQ ID NO: 190
		Probe	CAAACAGATTCAGATGGTCCGGCA	SEQ ID NO: 191
		Reverse Primer	TCTCCATATCGGCCTTTACC	SEQ ID NO: 192
BRAF	NM_004333.1	Forward Primer	CCTTCCGACCAGCAGATGAA	SEQ ID NO: 193
		Probe	CAATTTGGGCAACGAGACCGATCCT	SEQ ID NO: 194
		Reverse Primer	TTTATATGCACATTGGGAGCTGAT	SEQ ID NO: 195
BRCA1	NM_007295.1	Forward Primer	TCAGGGGGCTAGAAATCTGT	SEQ ID NO: 196
		Probe	CTATGGGCCCTTCACCAACATGC	SEQ ID NO: 197
		Reverse Primer	CCATTCCAGTTGATCTGTGG	SEQ ID NO: 198
BRCA2	NM_000059.1	Forward Primer	AGTTCGTGCTTTGCAAGATG	SEQ ID NO: 199
		Probe	CATTCTTCACTGCTTCATAAAGCTCTGCA	SEQ ID NO: 200
		Reverse Primer	AAGGTAAGCTGGGTCTGCTG	SEQ ID NO: 201
BRK	NM_005975.1	Forward Primer	GTGCAGGAAAGGTTCACAAA	SEQ ID NO: 202
		Probe	AGTGTCTGCGTCCAATACACGCGT	SEQ ID NO: 203
		Reverse Primer	GCACACACGATGGAGTAAGG	SEQ ID NO: 204
BTF3	NM_001207.2	Forward Primer	CAGTGATCCACTTTAACAACCCTAAAG	SEQ ID NO: 205
		Probe	TCAGGCATCTCTGGCAGCGAACAC	SEQ ID NO: 206
		Reverse Primer	AGCATGGCCTGTAATGGTGAA	SEQ ID NO: 207
BTRC	NM_033637.2	Forward Primer	GTTGGGACACAGTTGGTCTG	SEQ ID NO: 208
		Probe	CAGTCGGCCCAGGACGGTCTACT	SEQ ID NO: 209
		Reverse Primer	TGAAGCAGTCAGTTGTGCTG	SEQ ID NO: 210
BUB1	NM_004336.1	Forward Primer	CCGAGGTTAATCCAGCACGTA	SEQ ID NO: 211
		Probe	TGCTGGGAGCCTACACTTGGCCC	SEQ ID NO: 212
		Reverse Primer	AAGACATGGCGCTCTCAGTTC	SEQ ID NO: 213
BUB1B	NM_001211.3	Forward Primer	TCAACAGAAGGCTGAACCACTAGA	SEQ ID NO: 214
		Probe	TACAGTCCCAGCACCGACAATTCC	SEQ ID NO: 215
		Reverse Primer	CAACAGAGTTTGCCGAGACACT	SEQ ID NO: 216
BUB3	NM_004725.1	Forward Primer	CTGAAGCAGATGGTTCATCATT	SEQ ID NO: 217
		Probe	CCTCGCTTTGTTTAACAGCCCAGG	SEQ ID NO: 218
		Reverse Primer	GCTGATTCCCAAGAGTCTAACC	SEQ ID NO: 219
c-abl	NM_005157.2	Forward Primer	CCATCTCGCTGAGATACGAA	SEQ ID NO: 220
		Probe	GGGAGGGTGTACCATTACAGGATCAACA	SEQ ID NO: 221
		Reverse Primer	AGACGTAGAGCTTGCCATCA	SEQ ID NO: 222
c-kit	NM_000222.1	Forward Primer	GAGGCAACTGCTTATGGCTTAATTA	SEQ ID NO: 223
		Probe	TTACAGCGACAGTCATGGCCGCAT	SEQ ID NO: 224
		Reverse Primer	GGCACTCGGCTTGAGCAT	SEQ ID NO: 225
c-myb (MYB official)	NM_005375.1	Forward Primer	AACTCAGACTTGGAAATGCCTTCT	SEQ ID NO: 226
		Probe	AACTTCCACCCCCCTCATTGGTCACA	SEQ ID NO: 227
		Reverse Primer	CTGGTCTCTATGAAATGGTGTTGTAAC	SEQ ID NO: 228
c-Src	NM_005417.3	Forward Primer	TGAGGAGTGGTATTTTGGCAAGA	SEQ ID NO: 229
		Probe	AACCGCTCTGACTCCCGTCTGGTG	SEQ ID NO: 230
		Reverse Primer	CTCTCGGGTTCTCTGCATTGA	SEQ ID NO: 231

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
C20 orf1	NM_012112.2	Forward Primer	TCAGCTGTGAGCTGCGGATA	SEQ ID NO: 232
		Probe	CAGGTCCCATTGCCGGGCG	SEQ ID NO: 233
		Reverse Primer	ACGGTCCTAGGTTTGAGGTTAAGA	SEQ ID NO: 234
C20ORF126	NM_030815.2	Forward Primer	CCAGCACTGCTCGTTACTGT	SEQ ID NO: 235
		Probe	TGGGACCTCAGACCACTGAAGGC	SEQ ID NO: 236
		Reverse Primer	TTGACTTCACGGCAGTTCATA	SEQ ID NO: 237
C8orf4	NM_020130.2	Forward Primer	CTACGAGTCAGCCCATCCAT	SEQ ID NO: 238
		Probe	CATGGCTACCACTTCGACACAGCC	SEQ ID NO: 239
		Reverse Primer	TGCCCACGGCTTTCTTAC	SEQ ID NO: 240
CA9	NM_001216.1	Forward Primer	ATCCTAGCCCTGGTTTTTGG	SEQ ID NO: 241
		Probe	TTTGCTGTCACCAGCGTCGC	SEQ ID NO: 242
		Reverse Primer	CTGCCTTCTCATCTGCACAA	SEQ ID NO: 243
Cad17	NM_004063.2	Forward Primer	GAAGGCCAAGAACCGAGTCA	SEQ ID NO: 244
		Probe	TTATATTCCAGTTTAAGGCCAATCCTC	SEQ ID NO: 245
		Reverse Primer	TCCCCAGTTAGTTCAAAAGTCACA	SEQ ID NO: 246
CALD1	NM_004342.4	Forward Primer	CACTAAGGTTTGAGACAGTTCCAGAA	SEQ ID NO: 247
		Probe	AACCCAAGCTCAAGACGCAGGACGAG	SEQ ID NO: 248
		Reverse Primer	GCGAATTAGCCCTCTACAACTGA	SEQ ID NO: 249
CAPG	NM_001747.1	Forward Primer	GATTGTCACTGATGGGGAGG	SEQ ID NO: 250
		Probe	AGGACCTGGATCATCTCAGCAGGC	SEQ ID NO: 251
		Reverse Primer	CCTTCAGAGCAGGCTTGG	SEQ ID NO: 252
CAPN1	NM_005186.2	Forward Primer	CAAGAAGCTGTACGAGCTCATCA	SEQ ID NO: 253
		Probe	CCGCTACTCGGAGCCCGACCTG	SEQ ID NO: 254
		Reverse Primer	GCAGCAAACGAAATTGTCAAAG	SEQ ID NO: 255
CASP8	NM_033357.1	Forward Primer	CCTCGGGGATACTGTCTGAT	SEQ ID NO: 256
		Probe	CAACAATCACAATTTTGCAAAAGCACG	SEQ ID NO: 257
		Reverse Primer	GAAGTTTGGGCACTTTCTCC	SEQ ID NO: 258
CASP9	NM_001229.2	Forward Primer	TGAATGCCGTGGATTGCA	SEQ ID NO: 259
		Probe	CACTAGCCCTGGACCAGCCACTGCT	SEQ ID NO: 260
		Reverse Primer	ACAGGGATCATGGGACACAAG	SEQ ID NO: 261
CAT	NM_001752.1	Forward Primer	ATCCATTCGATCTCACCAAGGT	SEQ ID NO: 262
		Probe	TGGCCTCACAAGGACTACCCTCTCATCC	SEQ ID NO: 263
		Reverse Primer	TCCGGTTTAAGACCAGTTTACCA	SEQ ID NO: 264
CAV1	NM_001753.3	Forward Primer	GTGGCTCAACATTGTGTTCC	SEQ ID NO: 265
		Probe	ATTTCAGCTGATCAGTGGGCCTCC	SEQ ID NO: 266
		Reverse Primer	CAATGGCCTCCATTTTACAG	SEQ ID NO: 267
CBL	NM_005188.1	Forward Primer	TCATTCACAAACCTGGCAGT	SEQ ID NO: 268
		Probe	TTCCGGCTGAGCTGTACTCGTCTG	SEQ ID NO: 269
		Reverse Primer	CATACCCAATAGCCCACTGA	SEQ ID NO: 270
CCL20	NM_004591.1	Forward Primer	CCATGTGCTGTACCAAGAGTTTG	SEQ ID NO: 271
		Probe	CAGCACTGACATCAAAGCAGCCAGGA	SEQ ID NO: 272
		Reverse Primer	CGCCGCAGAGGTGGAGTA	SEQ ID NO: 273
CCL3	NM_002983.1	Forward Primer	AGCAGACAGTGGTCAGTCCTT	SEQ ID NO: 274
		Probe	CTCTGCTGACACTCGAGCCCACAT	SEQ ID NO: 275
		Reverse Primer	CTGCATGATTCTGAGCAGGT	SEQ ID NO: 276
CCNA2	NM_001237.2	Forward Primer	CCATACCTCAAGTATTTGCCATCAG	SEQ ID NO: 277
		Probe	ATTGCTGGAGCTGCCTTTCATTTAGCACT	SEQ ID NO: 278
		Reverse Primer	AGCTTTGTCCCGTGACTGTGTA	SEQ ID NO: 279
CCNB1	NM_031966.1	Forward Primer	TTCAGGTTGTTGCAGGAGAC	SEQ ID NO: 280
		Probe	TGTCTCCATTATTGATCGGTTCATGCA	SEQ ID NO: 281
		Reverse Primer	CATCTTCTTGGGCACACAAT	SEQ ID NO: 282
CCNB2	NM_004701.2	Forward Primer	AGGCTTCTGCAGGAGACTCTGT	SEQ ID NO: 283
		Probe	TCGATCCATAATGCCAACGCACATG	SEQ ID NO: 284
		Reverse Primer	GGGAAACTGGCTGAACCTGTAA	SEQ ID NO: 285
CCND1	NM_001758.1	Forward Primer	GCATGTTCGTGGCCTCTAAGA	SEQ ID NO: 286
		Probe	AAGGAGACCATCCCCCTGACGGC	SEQ ID NO: 287
		Reverse Primer	CGGTGTAGATGCACAGCTTCTC	SEQ ID NO: 288

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
CCND3	NM_001760.2	Forward Primer	CCTCTGTGCTACAGATTATACCTTTGC	SEQ ID NO: 289
		Probe	TACCCGCCATCCATGATCGCCA	SEQ ID NO: 290
		Reverse Primer	CACTGCAGCCCCAATGCT	SEQ ID NO: 291
CCNE1	NM_001238.1	Forward Primer	AAAGAAGATGATGACCGGGTTTAC	SEQ ID NO: 292
		Probe	CAAACTCAACGTGCAAGCCTCGGA	SEQ ID NO: 293
		Reverse Primer	GAGCCTCTGGATGGTGCAAT	SEQ ID NO: 294
CCNE2	NM_057749.1	Forward Primer	GGTCACCAAGAAACATCAGTATGAA	SEQ ID NO: 295
		Probe	CCCAGATAATACAGGTGGCCAACAATTCCT	SEQ ID NO: 296
		Reverse Primer	TTCAATGATAATGCAAGGACTGATC	SEQ ID NO: 297
CCNE2 variant 1	NM_057749var1	Forward Primer	ATGCTGTGGCTCCTTCCTAACT	SEQ ID NO: 298
		Probe	TACCAAGCAACCTACATGTCAAGAAAGCCC	SEQ ID NO: 299
		Reverse Primer	ACCCAAATTGTGATATACAAAAAGGTT	SEQ ID NO: 300
CCR7	NM_001838.2	Forward Primer	GGATGACATGCACTCAGCTC	SEQ ID NO: 301
		Probe	CTCCCATCCCAGTGGAGCCAA	SEQ ID NO: 302
		Reverse Primer	CCTGACATTTCCCTTGTCCT	SEQ ID NO: 303
CD105	NM_000118.1	Forward Primer	GCAGGTGTCAGCAAGTATGATCAG	SEQ ID NO: 304
		Probe	CGACAGGATATTGACCACCGCCTCATT	SEQ ID NO: 305
		Reverse Primer	TTTTTCCGCTGTGGTGATGA	SEQ ID NO: 306
CD134 (TNFRSF4 official)	NM_003327.1	Forward Primer	GCCCAGTGCGGAGAACAG	SEQ ID NO: 307
		Probe	CCAGCTTGATTCTCGTCTCTGCACTTAAGC	SEQ ID NO: 308
		Reverse Primer	AATCACACGCACCTGGAGAAC	SEQ ID NO: 309
CD18	NM_000211.1	Forward Primer	CGTCAGGACCCACCATGTCT	SEQ ID NO: 310
		Probe	CGCGGCCGAGACATGGCTTG	SEQ ID NO: 311
		Reverse Primer	GGTTAATTGGTGACATCCTCAAGA	SEQ ID NO: 312
CD24	NM_013230.1	Forward Primer	TCCAACTAATGCCACCACCAA	SEQ ID NO: 313
		Probe	CTGTTGACTGCAGGGCACCACCA	SEQ ID NO: 314
		Reverse Primer	GAGAGAGTGAGACCACGAAGAGACT	SEQ ID NO: 315
CD28	NM_006139.1	Forward Primer	TGTGAAAGGGAAACACCTTTG	SEQ ID NO: 316
		Probe	CCAAGTCCCCTATTTCCCGGACCT	SEQ ID NO: 317
		Reverse Primer	AGCACCCAAAAGGGCTTAG	SEQ ID NO: 318
CD31	NM_000442.1	Forward Primer	TGTATTTCAAGACCTCTGTGCACTT	SEQ ID NO: 319
		Probe	TTTATGAACCTGCCCTGCTCCCACA	SEQ ID NO: 320
		Reverse Primer	TTAGCCTGAGGAATTGCTGTGTT	SEQ ID NO: 321
CD34	NM_001773.1	Forward Primer	CCACTGCACACACCTCAGA	SEQ ID NO: 322
		Probe	CTGTTCTTGGGGCCCTACACCTTG	SEQ ID NO: 323
		Reverse Primer	CAGGAGTTTACCTGCCCCT	SEQ ID NO: 324
CD3z	NM_000734.1	Forward Primer	AGATGAAGTGGAAGGCGCTT	SEQ ID NO: 325
		Probe	CACCGCGGCCATCCTGCA	SEQ ID NO: 326
		Reverse Primer	TGCCTCTGTAATCGGCAACTG	SEQ ID NO: 327
CD44E	X55150	Forward Primer	ATCACCGACAGCACAGACA	SEQ ID NO: 328
		Probe	CCCTGCTACCAATATGGACTCCAGTCA	SEQ ID NO: 329
		Reverse Primer	ACCTGTGTTTGGATTTGCAG	SEQ ID NO: 330
CD44s	M59040.1	Forward Primer	GACGAAGACAGTCCCTGGAT	SEQ ID NO: 331
		Probe	CACCGACAGCACAGACAGAATCCC	SEQ ID NO: 332
		Reverse Primer	ACTGGGGTGGAATGTGTCTT	SEQ ID NO: 333
CD44v3	AJ251595v3	Forward Primer	CACACAAAACAGAACCAGGACT	SEQ ID NO: 334
		Probe	ACCCAGTGGAACCCAAGCCATTC	SEQ ID NO: 335
		Reverse Primer	CTGAAGTAGCACTTCCGGATT	SEQ ID NO: 336
CD44v6	AJ251595v6	Forward Primer	CTCATACCAGCCATCCAATG	SEQ ID NO: 337
		Probe	CACCAAGCCCAGAGGACAGTTCCT	SEQ ID NO: 338
		Reverse Primer	TTGGGTTGAAGAAATCAGTCC	SEQ ID NO: 339
CD68	NM_001251.1	Forward Primer	TGGTTCCCAGCCCTGTGT	SEQ ID NO: 340
		Probe	CTCCAAGCCCAGATTCAGATTCGAGTCA	SEQ ID NO: 341
		Reverse Primer	CTCCTCCACCCTGGGTTGT	SEQ ID NO: 342
CD80	NM_005191.2	Forward Primer	TTCAGTTGCTTTGCAGGAAG	SEQ ID NO: 343
		Probe	TTCTGTGCCCACCATATTCCTCTAGACA	SEQ ID NO: 344
		Reverse Primer	TTGATCAAGGTCACCAGAGC	SEQ ID NO: 345

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
CD82	NM_002231.2	Forward Primer	GTGCAGGCTCAGGTGAAGTG	SEQ ID NO: 346
		Probe	TCAGCTTCTACAACTGGACAGACAACGCTG	SEQ ID NO: 347
		Reverse Primer	GACCTCAGGGCGATTCATGA	SEQ ID NO: 348
CD8A	NM_171827.1	Forward Primer	AGGGTGAGGTGCTTGAGTCT	SEQ ID NO: 349
		Probe	CCAACGGCAAGGGAACAAGTACTTCT	SEQ ID NO: 350
		Reverse Primer	GGGCACAGTATCCCAGGTA	SEQ ID NO: 351
CD9	NM_001769.1	Forward Primer	GGGCGTGGAACAGTTTATCT	SEQ ID NO: 352
		Probe	AGACATCTGCCCCAAGAAGGACGT	SEQ ID NO: 353
		Reverse Primer	CACGGTGAAGGTTTCGAGT	SEQ ID NO: 354
CDC2	NM_001786.2	Forward Primer	GAGAGCGACGCGGTTGTT	SEQ ID NO: 355
		Probe	TAGCTGCCGCTGCGGCCG	SEQ ID NO: 356
		Reverse Primer	GTATGGTAGATCCCGGCTTATTATTC	SEQ ID NO: 357
CDC20	NM_001255.1	Forward Primer	TGGATTGGAGTTCTGGGAATG	SEQ ID NO: 358
		Probe	ACTGGCCGTGGCACTGGACAACA	SEQ ID NO: 359
		Reverse Primer	GCTTGCACTCCACAGGTACACA	SEQ ID NO: 360
cdc25A	NM_001789.1	Forward Primer	TCTTGCTGGCTACGCCTCTT	SEQ ID NO: 361
		Probe	TGTCCCTGTTAGACGTCCTCCGTCCATA	SEQ ID NO: 362
		Reverse Primer	CTGCATTGTGGCACAGTTCTG	SEQ ID NO: 363
CDC25B	NM_021874.1	Forward Primer	AAACGAGCAGTTTGCCATCAG	SEQ ID NO: 364
		Probe	CCTCACCGGCATAGACTGGAAGCG	SEQ ID NO: 365
		Reverse Primer	GTTGGTGATGTTCCGAAGCA	SEQ ID NO: 366
CDC25C	NM_001790.2	Forward Primer	GGTGAGCAGAAGTGGCCTAT	SEQ ID NO: 367
		Probe	CTCCCCGTCGATGCCAGAGAACT	SEQ ID NO: 368
		Reverse Primer	CTTCAGTCTTGGCCTGTTCA	SEQ ID NO: 369
CDC4	NM_018315.2	Forward Primer	GCAGTCCGCTGTGTTCAA	SEQ ID NO: 370
		Probe	TGCTCCACTAACAACCCTCCTGCC	SEQ ID NO: 371
		Reverse Primer	GGATCCCACACCTTTACCATAA	SEQ ID NO: 372
CDC42	NM_001791.2	Forward Primer	TCCAGAGACTGCTGAAAA	SEQ ID NO: 373
		Probe	CCCGTGACCTGAAGGCTGTCAAG	SEQ ID NO: 374
		Reverse Primer	TGTGTAAGTGCAGAACAC	SEQ ID NO: 375
CDC42BPA	NM_003607.2	Forward Primer	GAGCTGAAAGACGCACACTG	SEQ ID NO: 376
		Probe	AATTCCTGCATGGCCAGTTTCCTC	SEQ ID NO: 377
		Reverse Primer	GCCGCTCATTGATCTCCA	SEQ ID NO: 378
CDC6	NM_001254.2	Forward Primer	GCAACACTCCCCATTTACCTC	SEQ ID NO: 379
		Probe	TTGTTCTCCACCAAAGCAAGGCAA	SEQ ID NO: 380
		Reverse Primer	TGAGGGGGACCATTCTCTTT	SEQ ID NO: 381
CDCA7 v2	NM_145810.1	Forward Primer	AAGACCGTGGATGGCTACAT	SEQ ID NO: 382
		Probe	ATGAAGATGACCTGCCCAGAAGCC	SEQ ID NO: 383
		Reverse Primer	AGGGTCACGGATGATCTGG	SEQ ID NO: 384
CDH1	NM_004360.2	Forward Primer	TGAGTGTCCCCCGGTATCTTC	SEQ ID NO: 385
		Probe	TGCCAATCCCGATGAAATTGGAAATTT	SEQ ID NO: 386
		Reverse Primer	CAGCCGCTTTCAGATTTTCAT	SEQ ID NO: 387
CDH11	NM_001797.2	Forward Primer	GTCGGCAGAAGCAGGACT	SEQ ID NO: 388
		Probe	CCTTCTGCCCATAGTGATCAGCGA	SEQ ID NO: 389
		Reverse Primer	CTACTCATGGGCGGGATG	SEQ ID NO: 390
CDH3	NM_001793.3	Forward Primer	ACCCATGTACCGTCCTCG	SEQ ID NO: 391
		Probe	CCAACCCAGATGAAATCGGCAACT	SEQ ID NO: 392
		Reverse Primer	CCGCCTTCAGGTTCTCAAT	SEQ ID NO: 393
CDK2	NM_001798.2	Forward Primer	AATGCTGCACTACGACCCTA	SEQ ID NO: 394
		Probe	CCTTGGCCGAAATCCGCTTGT	SEQ ID NO: 395
		Reverse Primer	TTGGTCACATCCTGGAAGAA	SEQ ID NO: 396
CDX1	NM_001804.1	Forward Primer	AGCAACACCAGCCTCCTG	SEQ ID NO: 397
		Probe	CACCTCCTCTCCAATGCCTGTGAA	SEQ ID NO: 398
		Reverse Primer	GGGCTATGGCAGAAACTCCT	SEQ ID NO: 399
Cdx2	NM_001265.2	Forward Primer	GGGCAGGCAAGGTTTACA	SEQ ID NO: 400
		Probe	ATCTTAGCTGCCTTTGGCTTCCGC	SEQ ID NO: 401
		Reverse Primer	GTCTTTGGTCAGTCCAGCTTTC	SEQ ID NO: 402

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
CEACAM1	NM_001712.2	Forward Primer	ACTTGCCTGTTCAGAGCACTCA	SEQ ID NO: 403
		Probe	TCCTTCCCACCCCCAGTCCTGTC	SEQ ID NO: 404
		Reverse Primer	TGGCAAATCCGAATTAGAGTGA	SEQ ID NO: 405
CEACAM6	NM_002483.2	Forward Primer	CACAGCCTCACTTCTAACCTTCTG	SEQ ID NO: 406
		Probe	ACCCACCCACCACTGCCAAGCTC	SEQ ID NO: 407
		Reverse Primer	TTGAATGGCGTGGATTCAATAG	SEQ ID NO: 408
CEBPB	NM_005194.2	Forward Primer	GCAACCCACGTGTAACTGTC	SEQ ID NO: 409
		Probe	CCGGGCCCTGAGTAATCGCTTAA	SEQ ID NO: 410
		Reverse Primer	ACAAGCCCGTAGGAACATCT	SEQ ID NO: 411
CEGP1	NM_020974.1	Forward Primer	TGACAATCAGCACACCTGCAT	SEQ ID NO: 412
		Probe	CAGGCCCTCTTCCGAGCGGT	SEQ ID NO: 413
		Reverse Primer	TGTGACTACAGCCGTGATCCTTA	SEQ ID NO: 414
CENPA	NM_001809.2	Forward Primer	TAAATTCACTCGTGGTGTGGA	SEQ ID NO: 415
		Probe	CTTCAATTGGCAAGCCCAGGC	SEQ ID NO: 416
		Reverse Primer	GCCTCTTGTAGGGCCAATAG	SEQ ID NO: 417
CENPE	NM_001813.1	Forward Primer	GGATGCTGGTGACCTCTTCT	SEQ ID NO: 418
		Probe	TCCCTCACGTTGCAACAGGAATTAA	SEQ ID NO: 419
		Reverse Primer	GCCAAGGCACCAAGTAACTC	SEQ ID NO: 420
CENPF	NM_016343.2	Forward Primer	CTCCCGTCAACAGCGTTC	SEQ ID NO: 421
		Probe	ACACTGGACCAGGAGTGCATCCAG	SEQ ID NO: 422
		Reverse Primer	GGGTGAGTCTGGCCTTCA	SEQ ID NO: 423
CES2	NM_003869.4	Forward Primer	ACTTTGCGAGAAATGGGAAC	SEQ ID NO: 424
		Probe	AGTGTGGCAGACCCTCGCCATT	SEQ ID NO: 425
		Reverse Primer	CAGGTATTGCTCCTCCTGGT	SEQ ID NO: 426
CGA (CHGA official)	NM_001275.2	Forward Primer	CTGAAGGAGCTCCAAGACCT	SEQ ID NO: 427
		Probe	TGCTGATGTGCCCTCTCCTTGG	SEQ ID NO: 428
		Reverse Primer	CAAAACCGCTGTGTTTCTTC	SEQ ID NO: 429
CGB	NM_000737.2	Forward Primer	CCACCATAGGCAGAGGCA	SEQ ID NO: 430
		Probe	ACACCCTACTCCCTGTGCCTCCAG	SEQ ID NO: 431
		Reverse Primer	AGTCGTCGAGTGCTAGGGAC	SEQ ID NO: 432
CHAF1B	NM_005441.1	Forward Primer	GAGGCCAGTGGTGGAAACAG	SEQ ID NO: 433
		Probe	AGCTGATGAGTCTGCCCTACCGCCTG	SEQ ID NO: 434
		Reverse Primer	TCCGAGGCCACAGCAAAC	SEQ ID NO: 435
CHD2	NM_001271.1	Forward Primer	CTCTGTGCGAGGCTGTCA	SEQ ID NO: 436
		Probe	ACCCATCTCGGGATCCCTGATACC	SEQ ID NO: 437
		Reverse Primer	GGTAAGGACTGTGGGCTGG	SEQ ID NO: 438
CHFR	NM_018223.1	Forward Primer	AAGGAAGTGGTCCCTCTGTG	SEQ ID NO: 439
		Probe	TGAAGTCTCCAGCTTTGCCTCAGC	SEQ ID NO: 440
		Reverse Primer	GACGCAGTCTTTCTGTCTGG	SEQ ID NO: 441
Chk1	NM_001274.1	Forward Primer	GATAAATTGGTACAAGGGATCAGCTT	SEQ ID NO: 442
		Probe	CCAGCCCACATGTCCTGATCATATGC	SEQ ID NO: 443
		Reverse Primer	GGGTGCCAAGTAACTGACTATTCA	SEQ ID NO: 444
Chk2	NM_007194.1	Forward Primer	ATGTGGAACCCCCACCTACTT	SEQ ID NO: 445
		Probe	AGTCCCAACAGAAACAAGAACTTCAGGCG	SEQ ID NO: 446
		Reverse Primer	CAGTCCACAGCACGGTTATACC	SEQ ID NO: 447
CIAP1	NM_001166.2	Forward Primer	TGCCTGTGGTGGGAAGCT	SEQ ID NO: 448
		Probe	TGACATAGCATCATCCTTTGGTTCCCAGTT	SEQ ID NO: 449
		Reverse Primer	GGAAAATGCCTCCGGTGTT	SEQ ID NO: 450
cIAP2	NM_001165.2	Forward Primer	GGATATTTCCGTGGCTCTTATTCA	SEQ ID NO: 451
		Probe	TCTCCATCAAATCCTGTAAACTCCAGAGCA	SEQ ID NO: 452
		Reverse Primer	CTTCTCATCAAGGCAGAAAAATCTT	SEQ ID NO: 453
CKS1B	NM_001826.1	Forward Primer	GGTCCCTAAAACCCATCTGA	SEQ ID NO: 454
		Probe	TGAACGCCAAGATTCCTCCATTCA	SEQ ID NO: 455
		Reverse Primer	TAATGGACCCATCCCTGACT	SEQ ID NO: 456
CKS2	NM_001827.1	Forward Primer	GGCTGGACGTGGTTTTGTCT	SEQ ID NO: 457
		Probe	CTGCGCCCGCTCTTCGCG	SEQ ID NO: 458
		Reverse Primer	CGCTGCAGAAAATGAAACGA	SEQ ID NO: 459

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
Claudin 4	NM_001305.2	Forward Primer	GGCTGCTTTGCTGCAACTG	SEQ ID NO: 460
		Probe	CGCACAGACAAGCCTTACTCCGCC	SEQ ID NO: 461
		Reverse Primer	CAGAGCGGGCAGCAGAATA	SEQ ID NO: 462
CLDN1	NM_021101.3	Forward Primer	TCTGGGAGGTGCCCTACTT	SEQ ID NO: 463
		Probe	TGTTCCTGTCCCCGAAAAACAACC	SEQ ID NO: 464
		Reverse Primer	TGGATAGGGCCTTGGTGTT	SEQ ID NO: 465
CLDN7	NM_001307.3	Forward Primer	GGTCTGCCCTAGTCATCCTG	SEQ ID NO: 466
		Probe	TGCACTGCTCTCCTGTTCCTGTCC	SEQ ID NO: 467
		Reverse Primer	GTACCCAGCCTTGCTCTCAT	SEQ ID NO: 468
CLIC1	NM_001288.3	Forward Primer	CGGTACTTGAGCAATGCCTA	SEQ ID NO: 469
		Probe	CGGGAAGAATTCGCTTCCACCTG	SEQ ID NO: 470
		Reverse Primer	TCGATCTCCTCATCATCTGG	SEQ ID NO: 471
CLTC	NM_004859.1	Forward Primer	ACCGTATGGACAGCCACAG	SEQ ID NO: 472
		Probe	TCTCACATGCTGTACCCAAAGCCA	SEQ ID NO: 473
		Reverse Primer	TGACTACAGGATCAGCGCTTC	SEQ ID NO: 474
CLU	NM_001831.1	Forward Primer	CCCCAGGATACCTACCACTACCT	SEQ ID NO: 475
		Probe	CCCTTCAGCCTGCCCCACCG	SEQ ID NO: 476
		Reverse Primer	TGCGGGACTTGGGAAAGA	SEQ ID NO: 477
cMet	NM_000245.1	Forward Primer	GACATTTCCAGTCCTGCAGTCA	SEQ ID NO: 478
		Probe	TGCCTCTCTGCCCCACCCTTTGT	SEQ ID NO: 479
		Reverse Primer	CTCCGATCGCACACATTTGT	SEQ ID NO: 480
cMYC	NM_002467.1	Forward Primer	TCCCTCCACTCGGAAGGACTA	SEQ ID NO: 481
		Probe	TCTGACACTGTCCAACTTGACCCTCTT	SEQ ID NO: 482
		Reverse Primer	CGGTTGTTGCTGATCTGTCTCA	SEQ ID NO: 483
CNN	NM_001299.2	Forward Primer	TCCACCCTCCTGGCTTTG	SEQ ID NO: 484
		Probe	TCCTTTCGTCTTCGCCATGCTGG	SEQ ID NO: 485
		Reverse Primer	TCACTCCCACGTTCACCTTGT	SEQ ID NO: 486
COL1A1	NM_000088.2	Forward Primer	GTGGCCATCCAGCTGACC	SEQ ID NO: 487
		Probe	TCCTGCGCCTGATGTCCACCG	SEQ ID NO: 488
		Reverse Primer	CAGTGGTAGGTGATGTTCTGGGA	SEQ ID NO: 489
COL1A2	NM_000089.2	Forward Primer	CAGCCAAGAACTGGTATAGGAGCT	SEQ ID NO: 490
		Probe	TCTCCTAGCCAGACGTGTTTCTTGTCCTTG	SEQ ID NO: 491
		Reverse Primer	AAACTGGCTGCCAGCATTG	SEQ ID NO: 492
COPS3	NM_003653.2	Forward Primer	ATGCCCAGTGTTCCTGACTT	SEQ ID NO: 493
		Probe	CGAAACGCTATTCTCACAGGTTCAGC	SEQ ID NO: 494
		Reverse Primer	CTCCCCATTACAAGTGCTGA	SEQ ID NO: 495
COX2	NM_000963.1	Forward Primer	TCTGCAGAGTTGGAAGCACTCTA	SEQ ID NO: 496
		Probe	CAGGATACAGCTCCACAGCATCGATGTC	SEQ ID NO: 497
		Reverse Primer	GCCGAGGCTTTTCTACCAGAA	SEQ ID NO: 498
COX3	MITO_COX3	Forward Primer	TCGAGTCTCCCTTCACCATT	SEQ ID NO: 499
		Probe	CGACGGCATCTACGGCTCAACAT	SEQ ID NO: 500
		Reverse Primer	GACGTGAAGTCCGTGGAAG	SEQ ID NO: 501
CP	NM_000096.1	Forward Primer	CGTGAGTACACAGATGCCTCC	SEQ ID NO: 502
		Probe	TCTTCAGGGCCTCTCTCCTTTCGA	SEQ ID NO: 503
		Reverse Primer	CCAGGATGCCAAGATGCT	SEQ ID NO: 504
CRBP	NM_002899.2	Forward Primer	TGGTCTGCAAGCAAGTATTCAAG	SEQ ID NO: 505
		Probe	TCTGCTTGGGCCTCACTGCACCT	SEQ ID NO: 506
		Reverse Primer	GCTGATTGGTTGGGACAAGGT	SEQ ID NO: 507
CREBBP	NM_004380.1	Forward Primer	TGGGAAGCAGCTGTGTACCAT	SEQ ID NO: 508
		Probe	CCTCGCGATGCTGCCTACTACAGCTATC	SEQ ID NO: 509
		Reverse Primer	GAAACACTTCTCACAGAAATGATACCTATT	SEQ ID NO: 510
CRIP2	NM_001312.1	Forward Primer	GTGCTACGCCACCCTGTT	SEQ ID NO: 511
		Probe	CCGATGTTCACGCCTTTGGGTC	SEQ ID NO: 512
		Reverse Primer	CAGGGGCTTCTCGTAGATGT	SEQ ID NO: 513
cripto (TDGF1 official)	NM_003212.1	Forward Primer	GGGTCTGTGCCCCATGAC	SEQ ID NO: 514
		Probe	CCTGGCTGCCCAAGAAGTGTTCCCT	SEQ ID NO: 515
		Reverse Primer	TGACCGTGCCAGCATTTACA	SEQ ID NO: 516

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
CRK(a)	NM_016823.2	Forward Primer	CTCCCTAACCTCCAGAATGG	SEQ ID NO: 517
		Probe	ACTCGCTTCTGGATAACCCTGGCA	SEQ ID NO: 518
		Reverse Primer	TGTCTTGTCGTAGGCATTGG	SEQ ID NO: 519
CRMP1	NM_001313.1	Forward Primer	AAGGTTTTTGGATTGCAAGG	SEQ ID NO: 520
		Probe	ACCGTCATACATGCCCCTGGAAAC	SEQ ID NO: 521
		Reverse Primer	GGGTGTAGCTGGTACCTCGT	SEQ ID NO: 522
CRYAB	NM_001885.1	Forward Primer	GATGTGATTGAGGTGCATGG	SEQ ID NO: 523
		Probe	TGTTCATCCTGGCGCTCTTCATGT	SEQ ID NO: 524
		Reverse Primer	GAACTCCCTGGAGATGAAACC	SEQ ID NO: 525
CSEL1	NM_001316.2	Forward Primer	TTACGCAGCTCATGCTCTTG	SEQ ID NO: 526
		Probe	ACGGCTCTTTACTATGCGAGGGCC	SEQ ID NO: 527
		Reverse Primer	GCAGCTGTAAAGAGAGTGGCAT	SEQ ID NO: 528
CSF1	NM_000757.3	Forward Primer	TGCAGCGGCTGATTGACA	SEQ ID NO: 529
		Probe	TCAGATGGAGACCTCGTGCCAAATTACA	SEQ ID NO: 530
		Reverse Primer	CAACTGTTCCTGGTCTACAAACTCA	SEQ ID NO: 531
CSK (SRC)	NM_004383.1	Forward Primer	CCTGAACATGAAGGAGCTGA	SEQ ID NO: 532
		Probe	TCCCGATGGTCTGCAGCAGCT	SEQ ID NO: 533
		Reverse Primer	CATCACGTCTCCGAACTCC	SEQ ID NO: 534
CTAG1B	NM_001327.1	Forward Primer	GCTCTCCATCAGCTCCTGTC	SEQ ID NO: 535
		Probe	CCACATCAACAGGGAAAGCTGCTG	SEQ ID NO: 536
		Reverse Primer	AACACGGGCAGAAAGCACT	SEQ ID NO: 537
CTGF	NM_001901.1	Forward Primer	GAGTTCAAGTGCCCTGACG	SEQ ID NO: 538
		Probe	AACATCATGTTCTTCTTCATGACCTCGC	SEQ ID NO: 539
		Reverse Primer	AGTTGTAATGGCAGGCACAG	SEQ ID NO: 540
CTHRC1	NM_138455.2	Forward Primer	GCTCACTTCGGCTAAAATGC	SEQ ID NO: 541
		Probe	ACCAACGCTGACAGCATGCATTTC	SEQ ID NO: 542
		Reverse Primer	TCAGCTCCATTGAATGTGAAA	SEQ ID NO: 543
CTLA4	NM_005214.2	Forward Primer	CACTGAGGTCCGGGTGACA	SEQ ID NO: 544
		Probe	CACCTGGCTGTCAGCCTGCCG	SEQ ID NO: 545
		Reverse Primer	GTAGGTTGCCGCACAGACTTC	SEQ ID NO: 546
CTNNBIP1	NM_020248.2	Forward Primer	GTTTTCCAGGTCGGAGACG	SEQ ID NO: 547
		Probe	CTTTGCAGCTACTGCCTCCGGTCT	SEQ ID NO: 548
		Reverse Primer	AGCATCCAGGGTGTTCCA	SEQ ID NO: 549
CTSB	NM_001908.1	Forward Primer	GGCCGAGATCTACAAAAACG	SEQ ID NO: 550
		Probe	CCCCGTGGAGGGAGCTTTCTC	SEQ ID NO: 551
		Reverse Primer	GCAGGAAGTCCGAATACACA	SEQ ID NO: 552
CTSD	NM_001909.1	Forward Primer	GTACATGATCCCCTGTGAGAAGGT	SEQ ID NO: 553
		Probe	ACCCTGCCCGCGATCACACTGA	SEQ ID NO: 554
		Reverse Primer	GGGACAGCTTGTAGCCTTTGC	SEQ ID NO: 555
CTSH	NM_004390.1	Forward Primer	GCAAGTTCCAACCTGGAAAG	SEQ ID NO: 556
		Probe	TGGCTACATCCTTGACAAAGCCGA	SEQ ID NO: 557
		Reverse Primer	CATCGCTTCCTCGTCATAGA	SEQ ID NO: 558
CTSL	NM_001912.1	Forward Primer	GGGAGGCTTATCTCACTGAGTGA	SEQ ID NO: 559
		Probe	TTGAGGCCCAGAGCAGTCTACCAGATTCT	SEQ ID NO: 560
		Reverse Primer	CCATTGCAGCCTTCATTGC	SEQ ID NO: 561
CTSL2	NM_001333.2	Forward Primer	TGTCTCACTGAGCGAGCAGAA	SEQ ID NO: 562
		Probe	CTTGAGGACGCGAACAGTCCACCA	SEQ ID NO: 563
		Reverse Primer	ACCATTGCAGCCCTGATTG	SEQ ID NO: 564
CUL1	NM_003592.2	Forward Primer	ATGCCCTGGTAATGTCTGCAT	SEQ ID NO: 565
		Probe	CAGCCACAAAGCCAGCGTCATTGT	SEQ ID NO: 566
		Reverse Primer	GCGACCACAAGCCTTATCAAG	SEQ ID NO: 567
CUL4A	NM_003589.1	Forward Primer	AAGCATCTTCCTGTTCTTGGA	SEQ ID NO: 568
		Probe	TATGTGCTGCAGAACTCCACGCTG	SEQ ID NO: 569
		Reverse Primer	AATCCCATATCCCAGATGGA	SEQ ID NO: 570
CXCL12	NM_000609.3	Forward Primer	GAGCTACAGATGCCCATGC	SEQ ID NO: 571
		Probe	TTCTTCGAAAGCCATGTTGCCAGA	SEQ ID NO: 572
		Reverse Primer	TTTGAGATGCTTGACGTTGG	SEQ ID NO: 573

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
CXCR4	NM_003467.1	Forward Primer	TGACCGCTTCTACCCCAATG	SEQ ID NO: 574
		Probe	CTGAAACTGGAACACAACCACCCACAAG	SEQ ID NO: 575
		Reverse Primer	AGGATAAGGCCAACCATGATGT	SEQ ID NO: 576
CYBA	NM_000101.1	Forward Primer	GGTGCCTACTCCATTGTGG	SEQ ID NO: 577
		Probe	TACTCCAGCAGGCACACAAACACG	SEQ ID NO: 578
		Reverse Primer	GTGGAGCCCTTCTTCCTCTT	SEQ ID NO: 579
CYP1B1	NM_000104.2	Forward Primer	CCAGCTTTGTGCCTGTCACTAT	SEQ ID NO: 580
		Probe	CTCATGCCACCACTGCCAACACCTC	SEQ ID NO: 581
		Reverse Primer	GGGAATGTGGTAGCCCAAGA	SEQ ID NO: 582
CYP2C8	NM_000770.2	Forward Primer	CCGTGTTCAAGAGGAAGCTC	SEQ ID NO: 583
		Probe	TTTTCTCAACTCCTCCACAAGGCA	SEQ ID NO: 584
		Reverse Primer	AGTGGGATCACAGGGTGAAG	SEQ ID NO: 585
CYP3A4	NM_017460.3	Forward Primer	AGAACAAGGACAACATAGATCCTTACATAT	SEQ ID NO: 586
		Probe	CACACCCTTTGGAAGTGGACCCAGAA	SEQ ID NO: 587
		Reverse Primer	GCAAACCTCATGCCAATGC	SEQ ID NO: 588
CYR61	NM_001554.3	Forward Primer	TGCTCATTCTTGAGGAGCAT	SEQ ID NO: 589
		Probe	CAGCACCCTTGGCAGTTTCGAAAT	SEQ ID NO: 590
		Reverse Primer	GTGGCTGCATTAGTGTCCAT	SEQ ID NO: 591
DAPK1	NM_004938.1	Forward Primer	CGCTGACATCATGAATGTTCCT	SEQ ID NO: 592
		Probe	TCATATCCAAACTCGCCTCCAGCCG	SEQ ID NO: 593
		Reverse Primer	TCTCTTTCAGCAACGATGTGTCTT	SEQ ID NO: 594
DCC	NM_005215.1	Forward Primer	AAATGTCCTCCTCGACTGCT	SEQ ID NO: 595
		Probe	ATCACTGGAACTCCTCGGTCGGAC	SEQ ID NO: 596
		Reverse Primer	TGAATGCCATCTTTCTTCCA	SEQ ID NO: 597
DCC_exons18-23	X76132_18-23	Forward Primer	GGTCACCGTTGGTGTCATCA	SEQ ID NO: 598
		Probe	CAGCCACGATGACCACTACCAGCACT	SEQ ID NO: 599
		Reverse Primer	GAGCGTCGGGTGCAAATC	SEQ ID NO: 600
DCC_exons6-7	X76132_6-7	Forward Primer	ATGGAGATGTGGTCATTCCTAGTG	SEQ ID NO: 601
		Probe	TGCTTCCTCCCACTATCTGAAAATAA	SEQ ID NO: 602
		Reverse Primer	CACCACCCCAAGTATCCGTAAG	SEQ ID NO: 603
DCK	NM_000788.1	Forward Primer	GCCGCCACAAGACTAAGGAAT	SEQ ID NO: 604
		Probe	AGCTGCCCGTCTTTCTCAGCCAGC	SEQ ID NO: 605
		Reverse Primer	CGATGTTCCCTTCGATGGAG	SEQ ID NO: 606
DDB1	NM_001923.2	Forward Primer	TGCGGATCATCCGGAATG	SEQ ID NO: 607
		Probe	AATTGGAATCCACGAGCATGCCAGC	SEQ ID NO: 608
		Reverse Primer	TCCTTTGATGCCTGGTAAGTCA	SEQ ID NO: 609
DET1	NM_017996.2	Forward Primer	CTTGTGGAGATCACCCAATCAG	SEQ ID NO: 610
		Probe	CTATGCCCGGGACTCGGGCCT	SEQ ID NO: 611
		Reverse Primer	CCCGCCTGGATCTCAAACT	SEQ ID NO: 612
DHFR	NM_000791.2	Forward Primer	TTGCTATAACTAAGTGCTTCTCCAAGA	SEQ ID NO: 613
		Probe	CCCAACTGAGTCCCCAGCACCT	SEQ ID NO: 614
		Reverse Primer	GTGGAATGGCAGCTCACTGTAG	SEQ ID NO: 615
DHPS	NM_013407.1	Forward Primer	GGGAGAACGGGATCAATAGGAT	SEQ ID NO: 616
		Probe	CTCATTGGGCACCAGCAGGTTTCC	SEQ ID NO: 617
		Reverse Primer	GCATCAGCCAGTCCTCAAACT	SEQ ID NO: 618
DIABLO	NM_019887.1	Forward Primer	CACAATGGCGGCTCTGAAG	SEQ ID NO: 619
		Probe	AAGTTACGCTGCGCGACAGCCAA	SEQ ID NO: 620
		Reverse Primer	ACACAAACACTGTCTGTACCTGAAGA	SEQ ID NO: 621
DIAPH1	NM_005219.2	Forward Primer	CAAGCAGTCAAGGAGAACCA	SEQ ID NO: 622
		Probe	TTCTTCTGTCTCCCGCCGCTTC	SEQ ID NO: 623
		Reverse Primer	AGTTTTGCTCGCCTCATCTT	SEQ ID NO: 624
DICER1	NM_177438.1	Forward Primer	TCCAATTCCAGCATCACTGT	SEQ ID NO: 625
		Probe	AGAAAAGCTGTTTGTCTCCCCAGCA	SEQ ID NO: 626
		Reverse Primer	GGCAGTGAAGGCGATAAAGT	SEQ ID NO: 627
DKK1	NM_012242.1	Forward Primer	TGACAACTACCAGCCGTACC	SEQ ID NO: 628
		Probe	AGTGCCGCACTCCTCGTCCTCT	SEQ ID NO: 629
		Reverse Primer	GGGACTAGCGCAGTACTCATC	SEQ ID NO: 630

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
DLC1	NM_006094.3	Forward Primer	GATTCAGACGAGGATGAGCC	SEQ ID NO: 631
		Probe	AAAGTCCATTTGCCACTGATGGCA	SEQ ID NO: 632
		Reverse Primer	CACCTCTTGCTGTCCCTTTG	SEQ ID NO: 633
DPYD	NM_000110.2	Forward Primer	AGGACGCAAGGAGGGTTTG	SEQ ID NO: 634
		Probe	CAGTGCCTACAGTCTCGAGTCTGCCAGTG	SEQ ID NO: 635
		Reverse Primer	GATGTCCGCCGAGTCCTTACT	SEQ ID NO: 636
DR4	NM_003844.1	Forward Primer	TGCACAGAGGGTGTGGGTTAC	SEQ ID NO: 637
		Probe	CAATGCTTCCAACAATTTGTTTGCTTGCC	SEQ ID NO: 638
		Reverse Primer	TCTTCATCTGATTTACAAGCTGTACATG	SEQ ID NO: 639
DR5	NM_003842.2	Forward Primer	CTCTGAGACAGTGCTTCGATGACT	SEQ ID NO: 640
		Probe	CAGACTTGGTGCCCTTTGACTCC	SEQ ID NO: 641
		Reverse Primer	CCATGAGGCCCAACTTCCT	SEQ ID NO: 642
DRG1	NM_004147.3	Forward Primer	CCTGGATCTCCCAGGTATCA	SEQ ID NO: 643
		Probe	ACCTTTCCCATCCTTGGCACCTTC	SEQ ID NO: 644
		Reverse Primer	TGCAATGACTTGACGACCTC	SEQ ID NO: 645
DSP	NM_004415.1	Forward Primer	TGGCACTACTGCATGATTGACA	SEQ ID NO: 646
		Probe	CAGGGCCATGACAATCGCCAA	SEQ ID NO: 647
		Reverse Primer	CCTGCCGCATTGTTTTCAG	SEQ ID NO: 648
DTYMK	NM_012145.1	Forward Primer	AAATCGCTGGGAACAAGTG	SEQ ID NO: 649
		Probe	CGCCCTGGCTCAACTTTTCCTTAA	SEQ ID NO: 650
		Reverse Primer	AATGCGTATCTGTCCACGAC	SEQ ID NO: 651
DUSP1	NM_004417.2	Forward Primer	AGACATCAGCTCCTGGTTCA	SEQ ID NO: 652
		Probe	CGAGGCCATTGACTTCATAGACTCCA	SEQ ID NO: 653
		Reverse Primer	GACAAACACCCTTCCTCCAG	SEQ ID NO: 654
DUSP2	NM_004418.2	Forward Primer	TATCCCTGTGGAGGACAACC	SEQ ID NO: 655
		Probe	CCTCCTGGAACCAGGCACTGATCT	SEQ ID NO: 656
		Reverse Primer	CACCCAGTCAATGAAGCCTA	SEQ ID NO: 657
DUT	NM_001948.2	Forward Primer	ACACATGGAGTGCTTCTGGA	SEQ ID NO: 658
		Probe	ATCAGCCCACTTGACCACCCAGTT	SEQ ID NO: 659
		Reverse Primer	CTCTTGCCTGTGCTTCCAC	SEQ ID NO: 660
DYRK1B	NM_004714.1	Forward Primer	AGCATGACACGGAGATGAAG	SEQ ID NO: 661
		Probe	CACCTGAAGCGGCACTTCATGTTC	SEQ ID NO: 662
		Reverse Primer	AATACCAGGCACAGGTGGTT	SEQ ID NO: 663
E2F1	NM_005225.1	Forward Primer	ACTCCCTCTACCCTTGAGCA	SEQ ID NO: 664
		Probe	CAGAAGAACAGCTCAGGGACCCCT	SEQ ID NO: 665
		Reverse Primer	CAGGCCTCAGTTCCTTCAGT	SEQ ID NO: 666
EDN1 endothelin	NM_001955.1	Forward Primer	TGCCACCTGGACATCATTTG	SEQ ID NO: 667
		Probe	CACTCCCGAGCACGTTGTTCCGT	SEQ ID NO: 668
		Reverse Primer	TGGACCTAGGGCTTCCAAGTC	SEQ ID NO: 669
EFNA1	NM_004428.2	Forward Primer	TACATCTCCAAACCCATCCA	SEQ ID NO: 670
		Probe	CAACCTCAAGCAGCGGTCTTCATG	SEQ ID NO: 671
		Reverse Primer	TTGCCACTGACAGTCACCTT	SEQ ID NO: 672
EFNA3	NM_004952.3	Forward Primer	ACTACATCTCCACGCCCACT	SEQ ID NO: 673
		Probe	CCTCAGACACTTCCAGTGCAGGTTG	SEQ ID NO: 674
		Reverse Primer	CAGCAGACGAACACCTTCAT	SEQ ID NO: 675
EFNB1	NM_004429.3	Forward Primer	GGAGCCCGTATCCTGGAG	SEQ ID NO: 676
		Probe	CCCTCAACCCCAAGTTCCTGAGTG	SEQ ID NO: 677
		Reverse Primer	GGATAGATCACCAAGCCCTTC	SEQ ID NO: 678
EFNB2	NM_004093.2	Forward Primer	TGACATTATCATCCCGCTAAGGA	SEQ ID NO: 679
		Probe	CGGACAGCGTCTTCTGCCCTCACT	SEQ ID NO: 680
		Reverse Primer	GTAGTCCCCGCTGACCTTCTC	SEQ ID NO: 681
EFP	NM_005082.2	Forward Primer	TTGAACAGAGCCTGACCAAG	SEQ ID NO: 682
		Probe	TGATGCTTTCTCCAGAAACTCGAACTCA	SEQ ID NO: 683
		Reverse Primer	TGTTGAGATTCCTCGCAGTT	SEQ ID NO: 684
EGFR	NM_005228.1	Forward Primer	TGTCGATGGACTTCCAGAAC	SEQ ID NO: 685
		Probe	CACCTGGGCAGCTGCCAA	SEQ ID NO: 686
		Reverse Primer	ATTGGGACAGCTTGGATCA	SEQ ID NO: 687

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
EGLN1	NM_022051.1	Forward Primer	TCAATGGCCGGACGAAAG	SEQ ID NO: 688
		Probe	CATTGCCCGGATAACAAGCAACCATG	SEQ ID NO: 689
		Reverse Primer	TTTGGATTATCAACATGACGTACATAAC	SEQ ID NO: 690
EGLN3	NM_022073.2	Forward Primer	GCTGGTCCTCTACTGCGG	SEQ ID NO: 691
		Probe	CCGGCTGGGCAAATACTACGTCAA	SEQ ID NO: 692
		Reverse Primer	CCACCATTGCCTTAGACCTC	SEQ ID NO: 693
EGR1	NM_001964.2	Forward Primer	GTCCCCGCTGCAGATCTCT	SEQ ID NO: 694
		Probe	CGGATCCTTTCCTCACTCGCCCA	SEQ ID NO: 695
		Reverse Primer	CTCCAGCTTAGGGTAGTTGTCCAT	SEQ ID NO: 696
EGR3	NM_004430.2	Forward Primer	CCATGTGGATGAATGAGGTG	SEQ ID NO: 697
		Probe	ACCCAGTCTCACCTTCTCCCCACC	SEQ ID NO: 698
		Reverse Primer	TGCCTGAGAAGAGGTGAGGT	SEQ ID NO: 699
EI24	NM_004879.2	Forward Primer	AAAGTGGTGAATGCCATTTG	SEQ ID NO: 700
		Probe	CCTCAAATGCCAGGTCAGCTATATCCTG	SEQ ID NO: 701
		Reverse Primer	GTGAGGCTTCCTCCCTGATA	SEQ ID NO: 702
EIF4E	NM_001968.1	Forward Primer	GATCTAAGATGGCGACTGTCGAA	SEQ ID NO: 703
		Probe	ACCACCCCTACTCCTAATCCCCCGACT	SEQ ID NO: 704
		Reverse Primer	TTAGATTCCGTTTTCTCCTCTTCTG	SEQ ID NO: 705
EIF4EL3	NM_004846.1	Forward Primer	AAGCCGCGGTTGAATGTG	SEQ ID NO: 706
		Probe	TGACCCTCTCCCTCTCTGGATGGCA	SEQ ID NO: 707
		Reverse Primer	TGACGCCAGCTTCAATGATG	SEQ ID NO: 708
ELAVL1	NM_001419.2	Forward Primer	GACAGGAGGCCTCTATCCTG	SEQ ID NO: 709
		Probe	CACCCCACCCTCCACCTCAATC	SEQ ID NO: 710
		Reverse Primer	GTGAGGTAGGTCTGGGGAAG	SEQ ID NO: 711
EMP1	NM_001423.1	Forward Primer	GCTAGTACTTTGATGCTCCCTTGAT	SEQ ID NO: 712
		Probe	CCAGAGAGCCTCCCTGCAGCCA	SEQ ID NO: 713
		Reverse Primer	GAACAGCTGGAGGCCAAGTC	SEQ ID NO: 714
EMR3	NM_032571.2	Forward Primer	TGGCCTACCTCTTCACCATC	SEQ ID NO: 715
		Probe	TCAACAGCCTCCAAGGCTTCTTCA	SEQ ID NO: 716
		Reverse Primer	TGAGGAGGCAGTAGACCAAGA	SEQ ID NO: 717
EMS1	NM_005231.2	Forward Primer	GGCAGTGTCACTGAGTCCTTGA	SEQ ID NO: 718
		Probe	ATCCTCCCCTGCCCCGCG	SEQ ID NO: 719
		Reverse Primer	TGCACTGTGCGTCCCAAT	SEQ ID NO: 720
ENO1	NM_001428.2	Forward Primer	CAAGGCCGTGAACGAGAAGT	SEQ ID NO: 721
		Probe	CTGCAACTGCCTCCTGCTCAAAGTCA	SEQ ID NO: 722
		Reverse Primer	CGGTCACGGAGCCAATCT	SEQ ID NO: 723
EP300	NM_001429.1	Forward Primer	AGCCCCAGCAACTACAGTCT	SEQ ID NO: 724
		Probe	CACTGACATCATGGCTGGCCTTG	SEQ ID NO: 725
		Reverse Primer	TGTTCAAAGGTTGACCATGC	SEQ ID NO: 726
EPAS1	NM_001430.3	Forward Primer	AAGCCTTGGAGGGTTTCATTG	SEQ ID NO: 727
		Probe	TGTCGCCATCTTGGGTCACCACG	SEQ ID NO: 728
		Reverse Primer	TGCTGATGTTTTCTGACAGAAAGAT	SEQ ID NO: 729
EpCAM	NM_002354.1	Forward Primer	GGGCCCTCCAGAACAATGAT	SEQ ID NO: 730
		Probe	CCGCTCTCATCGCAGTCAGGATCAT	SEQ ID NO: 731
		Reverse Primer	TGCACTGCTTGGCCTTAAAGA	SEQ ID NO: 732
EPHA2	NM_004431.2	Forward Primer	CGCCTGTTCACCAAGATTGAC	SEQ ID NO: 733
		Probe	TGCGCCCGATGAGATCACCG	SEQ ID NO: 734
		Reverse Primer	GTGGCGTGCCTCGAAGTC	SEQ ID NO: 735
EPHB2	NM_004442.4	Forward Primer	CAACCAGGCAGCTCCATC	SEQ ID NO: 736
		Probe	CACCTGATGCATGATGGACACTGC	SEQ ID NO: 737
		Reverse Primer	GTAATGCTGTCCACGGTGC	SEQ ID NO: 738
EPHB4	NM_004444.3	Forward Primer	TGAACGGGGTATCCTCCTTA	SEQ ID NO: 739
		Probe	CGTCCCATTTGAGCCTGTCAATGT	SEQ ID NO: 740
		Reverse Primer	AGGTACCTCTCGGTCAGTGG	SEQ ID NO: 741
EphB6	NM_004445.1	Forward Primer	ACTGGTCCTCCATCGGCT	SEQ ID NO: 742
		Probe	CCTTGCACCTCAAACCAAAGCTCC	SEQ ID NO: 743
		Reverse Primer	CCAGTGTAGCATGAGTGCTGA	SEQ ID NO: 744

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
EPM2A	NM_005670.2	Forward Primer	ACTGTGGCACTTAGGGGAGA	SEQ ID NO: 745
		Probe	CTGCCTCTGCCCAAAGCAAATGTC	SEQ ID NO: 746
		Reverse Primer	AGTGGAAATGTGTCCTGGCT	SEQ ID NO: 747
ErbB3	NM_001982.1	Forward Primer	CGGTTATGTCATGCCAGATACAC	SEQ ID NO: 748
		Probe	CCTCAAAGGTACTCCCTCCTCCCGG	SEQ ID NO: 749
		Reverse Primer	GAACTGAGACCCACTGAAGAAAGG	SEQ ID NO: 750
ERCC1	NM_001983.1	Forward Primer	GTCCAGGTGGATGTGAAAGA	SEQ ID NO: 751
		Probe	CAGCAGGCCCTCAAGGAGCTG	SEQ ID NO: 752
		Reverse Primer	CGGCCAGGATACACATCTTA	SEQ ID NO: 753
ERCC2	NM_000400.2	Forward Primer	TGGCCTTCTTCACCAGCTA	SEQ ID NO: 754
		Probe	AGGCCACGGTGCTCTCCATGTACT	SEQ ID NO: 755
		Reverse Primer	CAAGGATCCCCTGCTCATAC	SEQ ID NO: 756
EREG	NM_001432.1	Forward Primer	ATAACAAAGTGTAGCTCTGACATGAATG	SEQ ID NO: 757
		Probe	TTGTTTGCATGGACAGTGCATCTATCTGGT	SEQ ID NO: 758
		Reverse Primer	CACACCTGCAGTAGTTTTGACTCA	SEQ ID NO: 759
ERK1	Z11696.1	Forward Primer	ACGGATCACAGTGGAGGAAG	SEQ ID NO: 760
		Probe	CGCTGGCTCACCCCTACCTG	SEQ ID NO: 761
		Reverse Primer	CTCATCCGTCGGGTCATAGT	SEQ ID NO: 762
ERK2	NM_002745.1	Forward Primer	AGTTCTTGACCCCTGGTCCT	SEQ ID NO: 763
		Probe	TCTCCAGCCCGTCTTGGCTT	SEQ ID NO: 764
		Reverse Primer	AAACGGCTCAAAGGAGTCAA	SEQ ID NO: 765
ESPL1	NM_012291.1	Forward Primer	ACCCCCAGACCGGATCAG	SEQ ID NO: 766
		Probe	CTGGCCCTCATGTCCCCTTCACG	SEQ ID NO: 767
		Reverse Primer	TGTAGGGCAGACTTCCTCAAACA	SEQ ID NO: 768
EstR1	NM_000125.1	Forward Primer	CGTGGTGCCCCTCTATGAC	SEQ ID NO: 769
		Probe	CTGGAGATGCTGGACGCCC	SEQ ID NO: 770
		Reverse Primer	GGCTAGTGGGCGCATGTAG	SEQ ID NO: 771
ETV4	NM_001986.1	Forward Primer	TCCAGTGCCTATGACCCC	SEQ ID NO: 772
		Probe	CAGACAAATCGCCATCAAGTCCCC	SEQ ID NO: 773
		Reverse Primer	ACTGTCCAAGGGCACCAG	SEQ ID NO: 774
F3	NM_001993.2	Forward Primer	GTGAAGGATGTGAAGCAGACGTA	SEQ ID NO: 775
		Probe	TGGCACGGGTCTTCTCCTACC	SEQ ID NO: 776
		Reverse Primer	AACCGGTGCTCTCCACATTC	SEQ ID NO: 777
FABP4	NM_001442.1	Forward Primer	GCTTTGCCACCAGGAAAGT	SEQ ID NO: 778
		Probe	CTGGCATGGCCAAACCTAACATGA	SEQ ID NO: 779
		Reverse Primer	CATCCCCATTCACACTGATG	SEQ ID NO: 780
FAP	NM_004460.2	Forward Primer	CTGACCAGAACCACGGCT	SEQ ID NO: 781
		Probe	CGGCCTGTCCACGAACCACTTATA	SEQ ID NO: 782
		Reverse Primer	GGAAGTGGGTCATGTGGG	SEQ ID NO: 783
fas	NM_000043.1	Forward Primer	GGATTGCTCAACAACCATGCT	SEQ ID NO: 784
		Probe	TCTGGACCCTCCTACCTCTGGTTCTTACGT	SEQ ID NO: 785
		Reverse Primer	GGCATTAACACTTTTGGACGATAA	SEQ ID NO: 786
fasl	NM_000639.1	Forward Primer	GCACTTTGGGATTCTTTCCATTAT	SEQ ID NO: 787
		Probe	ACAACATTCTCGGTGCCTGTAACAAAGAA	SEQ ID NO: 788
		Reverse Primer	GCATGTAAGAAGACCCTCACTGAA	SEQ ID NO: 789
FASN	NM_004104.4	Forward Primer	GCCTCTTCCTGTTCGACG	SEQ ID NO: 790
		Probe	TCGCCCACCTACGTACTGGCCTAC	SEQ ID NO: 791
		Reverse Primer	GCTTTGCCCGGTAGCTCT	SEQ ID NO: 792
FBXO5	NM_012177.2	Forward Primer	GGCTATTCCTCATTTTCTCTACAAAGTG	SEQ ID NO: 793
		Probe	CCTCCAGGAGGCTACCTTCTTCATGTTCAC	SEQ ID NO: 794
		Reverse Primer	GGATTGTAGACTGTCACCGAAATTC	SEQ ID NO: 795
FBXW7	NM_033632.1	Forward Primer	CCCCAGTTTCAACGAGACTT	SEQ ID NO: 796
		Probe	TCATTGCTCCCTAAAGAGTTGGCACTC	SEQ ID NO: 797
		Reverse Primer	GTTCCAGGAATGAAAGCACA	SEQ ID NO: 798
FDXR	NM_004110.2	Forward Primer	GAGATGATTCAGTTACCGGGAG	SEQ ID NO: 799
		Probe	AATCCACAGGATCCAAAATGGGCC	SEQ ID NO: 800
		Reverse Primer	ATCTTGTCCTGGAGACCCAA	SEQ ID NO: 801

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
FES	NM_002005.2	Forward Primer	CTCTGCAGGCCTAGGTGC	SEQ ID NO: 802
		Probe	CTCCTCAGCGGCTCCAGCTCATAT	SEQ ID NO: 803
		Reverse Primer	CCAGGACTGTGAAGAGCTGTC	SEQ ID NO: 804
FGF18	NM_003862.1	Forward Primer	CGGTAGTCAAGTCCGGATCAA	SEQ ID NO: 805
		Probe	CAAGGAGACGGAATTCTACCTGTGC	SEQ ID NO: 806
		Reverse Primer	GCTTGCCTTTGCGGTTCA	SEQ ID NO: 807
FGF2	NM_002006.2	Forward Primer	AGATGCAGGAGAGAGGAAGC	SEQ ID NO: 808
		Probe	CCTGCAGACTGCTTTTTGCCCAAT	SEQ ID NO: 809
		Reverse Primer	GTTTTGCAGCCTTACCCAAT	SEQ ID NO: 810
FGFR1	NM_023109.1	Forward Primer	CACGGGACATTCACCACATC	SEQ ID NO: 811
		Probe	ATAAAAAGACAACCAACGGCCGACTGC	SEQ ID NO: 812
		Reverse Primer	GGGTGCCATCCACTTCACA	SEQ ID NO: 813
FGFR2 isoform 1	NM_000141.2	Forward Primer	GAGGGACTGTTGGCATGCA	SEQ ID NO: 814
		Probe	TCCCAGAGACCAACGTTCAAGCAGTTG	SEQ ID NO: 815
		Reverse Primer	GAGTGAGAATTCGATCCAAGTCTTC	SEQ ID NO: 816
FHIT	NM_002012.1	Forward Primer	CCAGTGGAGCGCTTCCAT	SEQ ID NO: 817
		Probe	TCGGCCACTTCATCAGGACGCAG	SEQ ID NO: 818
		Reverse Primer	CTCTCTGGGTCGTCTGAAACAA	SEQ ID NO: 819
FIGF	NM_004469.2	Forward Primer	GGTTCCAGCTTTCTGTAGCTGT	SEQ ID NO: 820
		Probe	ATTGGTGGCCACACCACCTCCTTA	SEQ ID NO: 821
		Reverse Primer	GCCGCAGGTTCTAGTTGCT	SEQ ID NO: 822
FLJ12455	NM_022078.1	Forward Primer	CCACCAGCATGAAGTTTCG	SEQ ID NO: 823
		Probe	ACCCCTCACAAAGGCCATGTCTGT	SEQ ID NO: 824
		Reverse Primer	GGCTGTCTGAAGCACAACTG	SEQ ID NO: 825
FLJ20712	AK000719.1	Forward Primer	GCCACACAAACATGCTCCT	SEQ ID NO: 826
		Probe	ATGTCTTTCCCAGCAGCTCTGCCT	SEQ ID NO: 827
		Reverse Primer	GCCACAGGAAACTTCCGA	SEQ ID NO: 828
FLT1	NM_002019.1	Forward Primer	GGCTCCCGAATCTATCTTTG	SEQ ID NO: 829
		Probe	CTACAGCACCAAGAGCGACGTGTG	SEQ ID NO: 830
		Reverse Primer	TCCCACAGCAATACTCCGTA	SEQ ID NO: 831
FLT4	NM_002020.1	Forward Primer	ACCAAGAAGCTGAGGACCTG	SEQ ID NO: 832
		Probe	AGCCCGCTGACCATGGAAGATCT	SEQ ID NO: 833
		Reverse Primer	CCTGGAAGCTGTAGCAGACA	SEQ ID NO: 834
FOS	NM_005252.2	Forward Primer	CGAGCCCTTTGATGACTTCCT	SEQ ID NO: 835
		Probe	TCCCAGCATCATCCAGGCCCAG	SEQ ID NO: 836
		Reverse Primer	GGAGCGGGCTGTCTCAGA	SEQ ID NO: 837
FOXO3A	NM_001455.1	Forward Primer	TGAAGTCCAGGACGATGATG	SEQ ID NO: 838
		Probe	CTCTACAGCAGCTCAGCCAGCCTG	SEQ ID NO: 839
		Reverse Primer	ACGGCTTGCTTACTGAAGGT	SEQ ID NO: 840
FPGS	NM_004957.3	Forward Primer	CAGCCCTGCCAGTTTGAC	SEQ ID NO: 841
		Probe	ATGCCGTCTTCTGCCCTAACCTGA	SEQ ID NO: 842
		Reverse Primer	GTTGCCTGTGGATGACACC	SEQ ID NO: 843
FRP1	NM_003012.2	Forward Primer	TTGGTACCTGTGGGTTAGCA	SEQ ID NO: 844
		Probe	TCCCCAGGGTAGAATTCAATCAGAGC	SEQ ID NO: 845
		Reverse Primer	CACATCCAAATGCAAACTGG	SEQ ID NO: 846
FST	NM_006350.2	Forward Primer	GTAAGTCGGATGAGCCTGTCTGT	SEQ ID NO: 847
		Probe	CCAGTGACAATGCCACTTATGCCAGC	SEQ ID NO: 848
		Reverse Primer	CAGCTTCCTTCATGGCACACT	SEQ ID NO: 849
Furin	NM_002569.1	Forward Primer	AAGTCCTCGATACGCACTATAGCA	SEQ ID NO: 850
		Probe	CCCGGATGGTCTCCACGTCAT	SEQ ID NO: 851
		Reverse Primer	CTGGCATGTGGCACATGAG	SEQ ID NO: 852
FUS	NM_004960.1	Forward Primer	GGATAATTCAGACAACAACACCATCT	SEQ ID NO: 853
		Probe	TCAATTGTAACATTCTCACCCAGGCCTTG	SEQ ID NO: 854
		Reverse Primer	TGAAGTAATCAGCCACAGACTCAAT	SEQ ID NO: 855
FUT1	NM_000148.1	Forward Primer	CCGTGCTCATTGCTAACCA	SEQ ID NO: 856
		Probe	TCTGTCCCTGAACTCCCAGAACCA	SEQ ID NO: 857
		Reverse Primer	CTGCCCAAAGCCAGATGTA	SEQ ID NO: 858

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
FUT3	NM_000149.1	Forward Primer	CAGTTCGGTCCAACAGAGAA	SEQ ID NO: 859
		Probe	AGCAGGCAACCACCATGTCATTTG	SEQ ID NO: 860
		Reverse Primer	TGCGAATTATATCCCGATGA	SEQ ID NO: 861
FUT6	NM_000150.1	Forward Primer	CGTGTGTCTCAAGACGATCC	SEQ ID NO: 862
		Probe	TGTGTACCCTAATGGGTCCCGCTT	SEQ ID NO: 863
		Reverse Primer	GGTCCCTGTGCTGTCTGG	SEQ ID NO: 864
FXYD5	NM_014164.4	Forward Primer	AGAGCACCAAAGCAGCTCAT	SEQ ID NO: 865
		Probe	CACTGATGACACCACGACGCTCTC	SEQ ID NO: 866
		Reverse Primer	GTGCTTGGGGATGGTCTCT	SEQ ID NO: 867
FYN	NM_002037.3	Forward Primer	GAAGCGCAGATCATGAAGAA	SEQ ID NO: 868
		Probe	CTGAAGCACGACAAGCTGGTCCAG	SEQ ID NO: 869
		Reverse Primer	CTCCTCAGACACCACTGCAT	SEQ ID NO: 870
FZD1	NM_003505.1	Forward Primer	GGTGCACCAGTTCTACCCTC	SEQ ID NO: 871
		Probe	ACTTGAGCTCAGCGGAACACTGCA	SEQ ID NO: 872
		Reverse Primer	GCGTACATGGAGCACAGGA	SEQ ID NO: 873
FZD2	NM_001466.2	Forward Primer	TGGATCCTCACCTGGTCG	SEQ ID NO: 874
		Probe	TGCGCTTCCACCTTCTTCACTGTC	SEQ ID NO: 875
		Reverse Primer	GCGCTGCATGTCTACCAA	SEQ ID NO: 876
FZD6	NM_003506.2	Forward Primer	AATGAGAGAGGTGAAAGCGG	SEQ ID NO: 877
		Probe	CGGAGCTAGCACCCCCAGGTTAAG	SEQ ID NO: 878
		Reverse Primer	AGGTTCACCACAGTCCTGTTC	SEQ ID NO: 879
G-Catenin	NM_002230.1	Forward Primer	TCAGCAGCAAGGGCATCAT	SEQ ID NO: 880
		Probe	CGCCCGCAGGCCTCATCCT	SEQ ID NO: 881
		Reverse Primer	GGTGGTTTTCTTGAGCGTGTACT	SEQ ID NO: 882
G1P2	NM_005101.1	Forward Primer	CAACGAATTCCAGGTGTCC	SEQ ID NO: 883
		Probe	CTGAGCAGCTCCATGTCGGTGTC	SEQ ID NO: 884
		Reverse Primer	GATCTGCGCCTTCAGCTC	SEQ ID NO: 885
GADD45	NM_001924.2	Forward Primer	GTGCTGGTGACGAATCCA	SEQ ID NO: 886
		Probe	TTCATCTCAATGGAAGGATCCTGCC	SEQ ID NO: 887
		Reverse Primer	CCCGGCAAAAACAAATAAGT	SEQ ID NO: 888
GADD45B	NM_015675.1	Forward Primer	ACCCTCGACAAGACCACACT	SEQ ID NO: 889
		Probe	AACTTCAGCCCCAGCTCCCAAGTC	SEQ ID NO: 890
		Reverse Primer	TGGGAGTTCATGGGTACAGA	SEQ ID NO: 891
GADD45G	NM_006705.2	Forward Primer	CGCGCTGCAGATCCATTT	SEQ ID NO: 892
		Probe	CGCTGATCCAGGCTTTCTGCTGC	SEQ ID NO: 893
		Reverse Primer	CGCACTATGTCGATGTCGTTCT	SEQ ID NO: 894
GAGE4	NM_001474.1	Forward Primer	GGAACAGGGTCACCCACAGA	SEQ ID NO: 895
		Probe	TCAGGACCATCTTCACACTCACACCCA	SEQ ID NO: 896
		Reverse Primer	GATTTGGCGGGTCCATCTC	SEQ ID NO: 897
GBP1	NM_002053.1	Forward Primer	TTGGGAAATATTTGGGCATT	SEQ ID NO: 898
		Probe	TTGGGACATTGTAGACTTGGCCAGAC	SEQ ID NO: 899
		Reverse Primer	AGAAGCTAGGGTGGTTGTCC	SEQ ID NO: 900
GBP2	NM_004120.2	Forward Primer	GCATGGGAACCATCAACCA	SEQ ID NO: 901
		Probe	CCATGGACCAACTTCACTATGTGACAGAGC	SEQ ID NO: 902
		Reverse Primer	TGAGGAGTTTGCCTTGATTCG	SEQ ID NO: 903
GCLC	NM_001498.1	Forward Primer	CTGTTGCAGGAAGGCATTGA	SEQ ID NO: 904
		Probe	CATCTCCTGGCCCAGCATGTT	SEQ ID NO: 905
		Reverse Primer	GTCAGTGGGTCTCTAATAAAGAGATGAG	SEQ ID NO: 906
GCLM	NM_002061.1	Forward Primer	TGTAGAATCAAACTCTTCATCATCAACTAG	SEQ ID NO: 907
		Probe	TGCAGTTGACATGGCCTGTTCAGTCC	SEQ ID NO: 908
		Reverse Primer	CACAGAATCCAGCTGTGCAACT	SEQ ID NO: 909
GCNT1	NM_001490.3	Forward Primer	TGGTGCTTGGAGCATAGAAG	SEQ ID NO: 910
		Probe	TGCCCTTCACAAAGGAAATCCCTG	SEQ ID NO: 911
		Reverse Primer	GCAACGTCCTCAGCATTTC	SEQ ID NO: 912
GDF15	NM_004864.1	Forward Primer	CGCTCCAGACCTATGATGACT	SEQ ID NO: 913
		Probe	TGTTAGCCAAAGACTGCCACTGCA	SEQ ID NO: 914
		Reverse Primer	ACAGTGGAAGGACCAGGACT	SEQ ID NO: 915

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
GIT1	NM_014030.2	Forward Primer	GTGTATGACGAGGTGGATCG	SEQ ID NO: 916
		Probe	AGCCAGCCACACTGCATCATTTTC	SEQ ID NO: 917
		Reverse Primer	ACCAGAGTGCTGTGGTTTTG	SEQ ID NO: 918
GJA1	NM_000165.2	Forward Primer	GTTCACTGGGGGTGTATGG	SEQ ID NO: 919
		Probe	ATCCCCTCCCTCTCCACCCATCTA	SEQ ID NO: 920
		Reverse Primer	AAATACCAACATGCACCTCTCTT	SEQ ID NO: 921
GJB2	NM_004004.3	Forward Primer	TGTCATGTACGACGGCTTCT	SEQ ID NO: 922
		Probe	AGGCGTTGCACTTCACCAGCC	SEQ ID NO: 923
		Reverse Primer	AGTCCACAGTGTTGGGACAA	SEQ ID NO: 924
GPX1	NM_000581.2	Forward Primer	GCTTATGACCGACCCCAA	SEQ ID NO: 925
		Probe	CTCATCACCTGGTCTCCGGTGTGT	SEQ ID NO: 926
		Reverse Primer	AAAGTTCCAGGCAACATCGT	SEQ ID NO: 927
GPX2	NM_002083.1	Forward Primer	CACACAGATCTCCTACTCCATCCA	SEQ ID NO: 928
		Probe	CATGCTGCATCCTAAGGCTCCTCAGG	SEQ ID NO: 929
		Reverse Primer	GGTCCAGCAGTGTCTCCTGAA	SEQ ID NO: 930
Grb10	NM_005311.2	Forward Primer	CTTCGCCTTTGCTGATTGC	SEQ ID NO: 931
		Probe	CTCCAAACGCCTGCCTGACGACTG	SEQ ID NO: 932
		Reverse Primer	CCATAACGCACATGCTCCAA	SEQ ID NO: 933
GRB14	NM_004490.1	Forward Primer	TCCCACTGAAGCCCTTTCAG	SEQ ID NO: 934
		Probe	CCTCCAAGCGAGTCCTTCTTCAACCG	SEQ ID NO: 935
		Reverse Primer	AGTGCCCAGGCGTAAACATC	SEQ ID NO: 936
GRB2	NM_002086.2	Forward Primer	GTCCATCAGTGCATGACGTT	SEQ ID NO: 937
		Probe	AGGCCACGTATAGTCCTAGCTGACGC	SEQ ID NO: 938
		Reverse Primer	AGCCCACTTGGTTTCTTGTT	SEQ ID NO: 939
GRB7	NM_005310.1	Forward Primer	CCATCTGCATCCATCTTGTT	SEQ ID NO: 940
		Probe	CTCCCCACCCTTGAGAAGTGCCT	SEQ ID NO: 941
		Reverse Primer	GGCCACCAGGGTATTATCTG	SEQ ID NO: 942
GRIK1	NM_000830.2	Forward Primer	GTTGGGTGCATCTCTCGG	SEQ ID NO: 943
		Probe	AATTCATGCCGAGATACAGCCGCT	SEQ ID NO: 944
		Reverse Primer	CGTGCTCCATCTTCCTAGCTT	SEQ ID NO: 945
GRO1	NM_001511.1	Forward Primer	CGAAAAGATGCTGAACAGTGACA	SEQ ID NO: 946
		Probe	CTTCCTCCTCCCTTCTGGTCAGTTGGAT	SEQ ID NO: 947
		Reverse Primer	TCAGGAACAGCCACCAGTGA	SEQ ID NO: 948
GRP	NM_002091.1	Forward Primer	CTGGGTCTCATAGAAGCAAAGGA	SEQ ID NO: 949
		Probe	AGAAACCACCAGCCACCTCAACCCA	SEQ ID NO: 950
		Reverse Primer	CCACGAAGGCTGCTGATTG	SEQ ID NO: 951
GRPR	NM_005314.1	Forward Primer	ATGCTGCTGGCCATTCCA	SEQ ID NO: 952
		Probe	CCGTGTTTTCTGACCTCCATCCCTTCC	SEQ ID NO: 953
		Reverse Primer	AGGTCTGGTTGGTGCTTTCCT	SEQ ID NO: 954
GSK3B	NM_002093.2	Forward Primer	GACAAGGACGGCAGCAAG	SEQ ID NO: 955
		Probe	CCAGGAGTTGCCACCACTGTTGTC	SEQ ID NO: 956
		Reverse Primer	TTGTGGCCTGTCTGGACC	SEQ ID NO: 957
GSTA3	NM_000847.3	Forward Primer	TCTCCAACTTCCCTCTGCTG	SEQ ID NO: 958
		Probe	AGGCCCTGAAAACCAGAATCAGCA	SEQ ID NO: 959
		Reverse Primer	ACTTCTTCACCGTGGGCA	SEQ ID NO: 960
GSTM1	NM_000561.1	Forward Primer	AAGCTATGAGGAAAAGAAGTACACGAT	SEQ ID NO: 961
		Probe	TCAGCCACTGGCTTCTGTCATAATCAGGAG	SEQ ID NO: 962
		Reverse Primer	GGCCCAGCTTGAATTTTTCA	SEQ ID NO: 963
GSTM3	NM_000849.3	Forward Primer	CAATGCCATCTTGCGCTACAT	SEQ ID NO: 964
		Probe	CTCGCAAGCACAACATGTGTGGTGAGA	SEQ ID NO: 965
		Reverse Primer	GTCCACTCGAATCTTTTCTTCTTCA	SEQ ID NO: 966
GSTp	NM_000852.2	Forward Primer	GAGACCCTGCTGTCCCAGAA	SEQ ID NO: 967
		Probe	TCCCACAATGAAGGTCTTGCCTCCCT	SEQ ID NO: 968
		Reverse Primer	GGTTGTAGTCAGCGAAGGAGATC	SEQ ID NO: 969
GSTT1	NM_000853.1	Forward Primer	CACCATCCCCACCCTGTCT	SEQ ID NO: 970
		Probe	CACAGCCGCCTGAAAGCCACAAT	SEQ ID NO: 971
		Reverse Primer	GGCCTCAGTGTGCATCATTCT	SEQ ID NO: 972

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
H2AFZ	NM_002106.2	Forward Primer	CCGGAAAGGCCAAGACAA	SEQ ID NO: 973
		Probe	CCCGCTCGCAGAGAGCCGG	SEQ ID NO: 974
		Reverse Primer	AATACGGCCCACTGGGAACT	SEQ ID NO: 975
HB-EGF	NM_001945.1	Forward Primer	GACTCCTTCGTCCCCAGTTG	SEQ ID NO: 976
		Probe	TTGGGCCTCCCATAATTGCTTTGCC	SEQ ID NO: 977
		Reverse Primer	TGGCACTTGAAGGCTCTGGTA	SEQ ID NO: 978
hCRA a	U78556.1	Forward Primer	TGACACCCTTACCTTCCTGAGAA	SEQ ID NO: 979
		Probe	TCTGCTTTCCGCGCTCCCAGG	SEQ ID NO: 980
		Reverse Primer	AAAAACACGAGTCAAAAATAGAAGTCACT	SEQ ID NO: 981
HDAC1	NM_004964.2	Forward Primer	CAAGTACCACAGCGATGACTACATTAA	SEQ ID NO: 982
		Probe	TTCTTGCGCTCCATCCGTCCAGA	SEQ ID NO: 983
		Reverse Primer	GCTTGCTGTACTCCGACATGTT	SEQ ID NO: 984
HDAC2	NM_001527.1	Forward Primer	GGTGGCTACACAATCCGTAA	SEQ ID NO: 985
		Probe	TGCAGTCTCATATGTCCAACATCGAGC	SEQ ID NO: 986
		Reverse Primer	TGGGAATCTCACAATCAAGG	SEQ ID NO: 987
HDGF	NM_004494.1	Forward Primer	TCCTAGGCATTCTGGACCTC	SEQ ID NO: 988
		Probe	CATTCCTACCCCTGATCCCAACCC	SEQ ID NO: 989
		Reverse Primer	GCTGTTGATGCTCCATCCTT	SEQ ID NO: 990
hENT1	NM_004955.1	Forward Primer	AGCCGTGACTGTTGAGGTC	SEQ ID NO: 991
		Probe	AAGTCCAGCATCGCAGGCAGC	SEQ ID NO: 992
		Reverse Primer	AAGTAACGTTCCCAGGTGCT	SEQ ID NO: 993
Hepsin	NM_002151.1	Forward Primer	AGGCTGCTGGAGGTCATCTC	SEQ ID NO: 994
		Probe	CCAGAGGCCGTTTCTTGGCCG	SEQ ID NO: 995
		Reverse Primer	CTTCCTGCGGCCACAGTCT	SEQ ID NO: 996
HER2	NM_004448.1	Forward Primer	CGGTGTGAGAAGTGCAGCAA	SEQ ID NO: 997
		Probe	CCAGACCATAGCACACTCGGGCAC	SEQ ID NO: 998
		Reverse Primer	CCTCTCGCAAGTGCTCCAT	SEQ ID NO: 999
Herstatin	AF177761.2	Forward Primer	CACCCTGTCCTATCCTTCCT	SEQ ID NO: 1000
		Probe	CCCTCTTGGGACCTAGTCTCTGCCT	SEQ ID NO: 1001
		Reverse Primer	GGCCAGGGGTAGAGAGTAGA	SEQ ID NO: 1002
HES6	NM_018645.3	Forward Primer	TTAGGGACCCTGCAGCTCT	SEQ ID NO: 1003
		Probe	TAGCTCCCTCCCTCCACCCACTC	SEQ ID NO: 1004
		Reverse Primer	CTACAAAATTCTTCCTCCTGCC	SEQ ID NO: 1005
HGF	M29145.1	Forward Primer	CCGAAATCCAGATGATGATG	SEQ ID NO: 1006
		Probe	CTCATGGACCCTGGTGCTACACG	SEQ ID NO: 1007
		Reverse Primer	CCCAAGGAATGAGTGGATTT	SEQ ID NO: 1008
HIF1A	NM_001530.1	Forward Primer	TGAACATAAAGTCTGCAACATGGA	SEQ ID NO: 1009
		Probe	TTGCACTGCACAGGCCACATTCAC	SEQ ID NO: 1010
		Reverse Primer	TGAGGTTGGTTACTGTTGGTATCATATA	SEQ ID NO: 1011
HK1	NM_000188.1	Forward Primer	TACGCACAGAGGCAAGCA	SEQ ID NO: 1012
		Probe	TAAGAGTCCGGGATCCCCAGCCTA	SEQ ID NO: 1013
		Reverse Primer	GAGAGAAGTGCTGGAGAGGC	SEQ ID NO: 1014
HLA-DPB1	NM_002121.4	Forward Primer	TCCATGATGGTTCTGCAGGTT	SEQ ID NO: 1015
		Probe	CCCCGGACAGTGGCTCTGACG	SEQ ID NO: 1016
		Reverse Primer	TGAGCAGCACCATCAGTAACG	SEQ ID NO: 1017
HLA-DRA	NM_019111.3	Forward Primer	GACGATTTGCCAGCTTTGAG	SEQ ID NO: 1018
		Probe	TCAAGGTGCATTGGCCAACATAGC	SEQ ID NO: 1019
		Reverse Primer	TCCAGGTTGGCTTTGTCC	SEQ ID NO: 1020
HLA-DRB1	NM_002124.1	Forward Primer	GCTTTCTCAGGACCTGGTTG	SEQ ID NO: 1021
		Probe	CATTTTCTGCAGTTGCCGAACCAG	SEQ ID NO: 1022
		Reverse Primer	AGGAAGCCACAAGGGAGG	SEQ ID NO: 1023
HLA-G	NM_002127.2	Forward Primer	CCTGCGCGGCTACTACAAC	SEQ ID NO: 1024
		Probe	CGAGGCCAGTTCTCACACCCTCCAG	SEQ ID NO: 1025
		Reverse Primer	CAGGTCGCAGCCAATCATC	SEQ ID NO: 1026
HMGB1	NM_002128.3	Forward Primer	TGGCCTGTCCATTGGTGAT	SEQ ID NO: 1027
		Probe	TTCCACATCTCTCCCAGTTTCTTCGCAA	SEQ ID NO: 1028
		Reverse Primer	GCTTGTCATCTGCAGCAGTGTT	SEQ ID NO: 1029

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
hMLH	NM_000249.2	Forward Primer	CTACTTCCAGCAACCCCAGA	SEQ ID NO: 1030
		Probe	TCCACATCAGAATCTTCCCG	SEQ ID NO: 1031
		Reverse Primer	CTTTCGGGAATCATCTTCCA	SEQ ID NO: 1032
HNRPAB	NM_004499.2	Forward Primer	CAAGGGAGCGACCAACTGA	SEQ ID NO: 1033
		Probe	CTCCATATCCAAACAAAGCATGTGTGCG	SEQ ID NO: 1034
		Reverse Primer	GTTTGCCAAGTTAAATTTGGTACATAAT	SEQ ID NO: 1035
HNRPD	NM_031370.2	Forward Primer	GCCAGTAAGAACGAGGAGGA	SEQ ID NO: 1036
		Probe	AAGGCCATTCAAACTCCTCCCCAC	SEQ ID NO: 1037
		Reverse Primer	CGTCGCTGCTTCAGAGTGT	SEQ ID NO: 1038
HoxA1	NM_005522.3	Forward Primer	AGTGACAGATGGACAATGCAAGA	SEQ ID NO: 1039
		Probe	TGAACTCCTTCCTGGAATACCCCA	SEQ ID NO: 1040
		Reverse Primer	CCGAGTCGCCACTGCTAAGT	SEQ ID NO: 1041
HoxA5	NM_019102.2	Forward Primer	TCCCTTGTGTTCCTTCTGTGAA	SEQ ID NO: 1042
		Probe	AGCCCTGTTCTCGTTGCCCTAATTCATC	SEQ ID NO: 1043
		Reverse Primer	GGCAATAAACAGGCTCATGATTAA	SEQ ID NO: 1044
HOXB13	NM_006361.2	Forward Primer	CGTGCCTTATGGTTACTTTGG	SEQ ID NO: 1045
		Probe	ACACTCGGCAGGAGTAGTACCCGC	SEQ ID NO: 1046
		Reverse Primer	CACAGGGTTTCAGCGAGC	SEQ ID NO: 1047
HOXB7	NM_004502.2	Forward Primer	CAGCCTCAAGTTCGGTTTTC	SEQ ID NO: 1048
		Probe	ACCGGAGCCTTCCCAGAACAAACT	SEQ ID NO: 1049
		Reverse Primer	GTTGGAAGCAAACGCACA	SEQ ID NO: 1050
HRAS	NM_005343.2	Forward Primer	GGACGAATACGACCCCACT	SEQ ID NO: 1051
		Probe	ACCACCTGCTTCCGGTAGGAATCC	SEQ ID NO: 1052
		Reverse Primer	GCACGTCTCCCCATCAAT	SEQ ID NO: 1053
HSBP1	NM_001537.1	Forward Primer	GGAGATGGCCGAGACTGAC	SEQ ID NO: 1054
		Probe	CAAGACCGTGCAGGACCTCACCT	SEQ ID NO: 1055
		Reverse Primer	CTGCAGGAGTGTCTGCACC	SEQ ID NO: 1056
HSD17B1	NM_000413.1	Forward Primer	CTGGACCGCACGGACATC	SEQ ID NO: 1057
		Probe	ACCGCTTCTACCAATACCTCGCCCA	SEQ ID NO: 1058
		Reverse Primer	CGCCTCGCGAAAGACTTG	SEQ ID NO: 1059
HSD17B2	NM_002153.1	Forward Primer	GCTTTCCAAGTGGGGAATTA	SEQ ID NO: 1060
		Probe	AGTTGCTTCCATCCAACCTGGAGG	SEQ ID NO: 1061
		Reverse Primer	TGCCTGCGATATTTGTTAGG	SEQ ID NO: 1062
HSPA1A	NM_005345.4	Forward Primer	CTGCTGCGACAGTCCACTA	SEQ ID NO: 1063
		Probe	AGAGTGACTCCCGTTGTCCCAAGG	SEQ ID NO: 1064
		Reverse Primer	CAGGTTCGCTCTGGGAAG	SEQ ID NO: 1065
HSPA1B	NM_005346.3	Forward Primer	GGTCCGCTTCGTCTTTCGA	SEQ ID NO: 1066
		Probe	TGACTCCCGCGGTCCCAAGG	SEQ ID NO: 1067
		Reverse Primer	GCACAGGTTCGCTCTGGAA	SEQ ID NO: 1068
HSPA4	NM_002154.3	Forward Primer	TTCAGTGTGTCCAGTGCATC	SEQ ID NO: 1069
		Probe	CATTTTCCTCAGACTTGTGAACCTCCACT	SEQ ID NO: 1070
		Reverse Primer	ATCTGTTTCCATTGGCTCCT	SEQ ID NO: 1071
HSPA5	NM_005347.2	Forward Primer	GGCTAGTAGAACTGGATCCCAACA	SEQ ID NO: 1072
		Probe	TAATTAGACCTAGGCCTCAGCTGCACTGCC	SEQ ID NO: 1073
		Reverse Primer	GGTCTGCCCAAATGCTTTTC	SEQ ID NO: 1074
HSPA8	NM_006597.3	Forward Primer	CCTCCCTCTGGTGGTGCTT	SEQ ID NO: 1075
		Probe	CTCAGGGCCCACCATTGAAGAGGTTG	SEQ ID NO: 1076
		Reverse Primer	GCTACATCTACACTTGGTTGGCTTAA	SEQ ID NO: 1077
HSPB1	NM_001540.2	Forward Primer	CCGACTGGAGGAGCATAAA	SEQ ID NO: 1078
		Probe	CGCACTTTTCTGAGCAGACGTCCA	SEQ ID NO: 1079
		Reverse Primer	ATGCTGGCTGACTCTGCTC	SEQ ID NO: 1080
HSPCA	NM_005348.2	Forward Primer	CAAAAGGCAGAGGCTGATAA	SEQ ID NO: 1081
		Probe	TGACCAGATCCTTCACAGACTTGTCGT	SEQ ID NO: 1082
		Reverse Primer	AGCGCAGTTTCATAAAGCAA	SEQ ID NO: 1083
HSPE1	NM_002157.1	Forward Primer	GCAAGCAACAGTAGTCGCTG	SEQ ID NO: 1084
		Probe	TCTCCACCCTTTCCTTTAGAACCCG	SEQ ID NO: 1085
		Reverse Primer	CCAACTTTCACGCTAACTGGT	SEQ ID NO: 1086

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
HSPG2	NM_005529.2	Forward Primer	GAGTACGTGTGCCGAGTGTT	SEQ ID NO: 1087
		Probe	CAGCTCCGTGCCTCTAGAGGCCT	SEQ ID NO: 1088
		Reverse Primer	CTCAATGGTGACCAGGACA	SEQ ID NO: 1089
ICAM1	NM_000201.1	Forward Primer	GCAGACAGTGACCATCTACAGCTT	SEQ ID NO: 1090
		Probe	CCGGCGCCCAACGTGATTCT	SEQ ID NO: 1091
		Reverse Primer	CTTCTGAGACCTCTGGCTTCGT	SEQ ID NO: 1092
ICAM2	NM_000873.2	Forward Primer	GGTCATCCTGACACTGCAAC	SEQ ID NO: 1093
		Probe	TTGCCCACAGCCACCAAAGTG	SEQ ID NO: 1094
		Reverse Primer	TGCACTCAATGGTGAAGGAC	SEQ ID NO: 1095
ID1	NM_002165.1	Forward Primer	AGAACCGCAAGGTGAGCAA	SEQ ID NO: 1096
		Probe	TGGAGATTCTCCAGCACGTCATCGAC	SEQ ID NO: 1097
		Reverse Primer	TCCAACTGAAGGTCCCTGATG	SEQ ID NO: 1098
ID2	NM_002166.1	Forward Primer	AACGACTGCTACTCCAAGCTCAA	SEQ ID NO: 1099
		Probe	TGCCCAGCATCCCCCAGAACAA	SEQ ID NO: 1100
		Reverse Primer	GGATTTCCATCTTGCTCACCTT	SEQ ID NO: 1101
ID3	NM_002167.2	Forward Primer	CTTCACCAAATCCCTTCCTG	SEQ ID NO: 1102
		Probe	TCACAGTCCTTCGCTCCTGAGCAC	SEQ ID NO: 1103
		Reverse Primer	CTCTGGCTCTTCAGGCTACA	SEQ ID NO: 1104
ID4	NM_001546.2	Forward Primer	TGGCCTGGCTCTTAATTTG	SEQ ID NO: 1105
		Probe	CTTTTGTTTTGCCCAGTATAGACTCGGAAG	SEQ ID NO: 1106
		Reverse Primer	TGCAATCATGCAAGACCAC	SEQ ID NO: 1107
IFIT1	NM_001548.1	Forward Primer	TGACAACCAAGCAAATGTGA	SEQ ID NO: 1108
		Probe	AAGTTGCCCCAGGTCACCAGACTC	SEQ ID NO: 1109
		Reverse Primer	CAGTCTGCCCATGTGGTAAT	SEQ ID NO: 1110
IGF1	NM_000618.1	Forward Primer	TCCGGAGCTGTGATCTAAGGA	SEQ ID NO: 1111
		Probe	TGTATTGCGCACCCCTCAAGCCTG	SEQ ID NO: 1112
		Reverse Primer	CGGACAGAGCGAGCTGACTT	SEQ ID NO: 1113
IGF1R	NM_000875.2	Forward Primer	GCATGGTAGCCGAAGATTTCA	SEQ ID NO: 1114
		Probe	CGCGTCATACCAAAATCTCCGATTTTGA	SEQ ID NO: 1115
		Reverse Primer	TTTCCGGTAATAGTCTGTCTCATAGATATC	SEQ ID NO: 1116
IGF2	NM_000612.2	Forward Primer	CCGTGCTTCCGGACAACTT	SEQ ID NO: 1117
		Probe	TACCCCGTGGGCAAGTTCTTCCAA	SEQ ID NO: 1118
		Reverse Primer	TGGACTGCTTCCAGGTGTCA	SEQ ID NO: 1119
IGFBP2	NM_000597.1	Forward Primer	GTGGACAGCACCATGAACA	SEQ ID NO: 1120
		Probe	CTTCCGGCCAGCACTGCCTC	SEQ ID NO: 1121
		Reverse Primer	CCTTCATACCCGACTTGAGG	SEQ ID NO: 1122
IGFBP3	NM_000598.1	Forward Primer	ACGCACCGGGTGTCTGA	SEQ ID NO: 1123
		Probe	CCCAAGTTCCACCCCCTCCATTCA	SEQ ID NO: 1124
		Reverse Primer	TGCCCTTTCTTGATGATGATTATC	SEQ ID NO: 1125
IGFBP5	NM_000599.1	Forward Primer	TGGACAAGTACGGGATGAAGCT	SEQ ID NO: 1126
		Probe	CCCGTCAACGTACTCCATGCCTGG	SEQ ID NO: 1127
		Reverse Primer	CGAAGGTGTGGCACTGAAAGT	SEQ ID NO: 1128
IGFBP6	NM_002178.1	Forward Primer	TGAACCGCAGAGACCAACAG	SEQ ID NO: 1129
		Probe	ATCCAGGCACCTCTACCACGCCCTC	SEQ ID NO: 1130
		Reverse Primer	GTCTTGGACACCCGCAGAAT	SEQ ID NO: 1131
IGFBP7	NM_001553	Forward Primer	GGGTCACTATGGAGTTCAAAGGA	SEQ ID NO: 1132
		Probe	CCCGGTCACCAGGCAGGAGTTCT	SEQ ID NO: 1133
		Reverse Primer	GGGTCTGAATGGCCAGGTT	SEQ ID NO: 1134
IHH	NM_002181.1	Forward Primer	AAGGACGAGGAGAACACAGG	SEQ ID NO: 1135
		Probe	ATGACCCAGCGCTGCAAGGAC	SEQ ID NO: 1136
		Reverse Primer	AGATAGCCAGCGAGTTCAGG	SEQ ID NO: 1137
IL-8	NM_000584.2	Forward Primer	AAGGAACCATCTCACTGTGTGTAAAC	SEQ ID NO: 1138
		Probe	TGACTTCCAAGCTGGCCGTGGC	SEQ ID NO: 1139
		Reverse Primer	ATCAGGAAGGCTGCCAAGAG	SEQ ID NO: 1140
IL10	NM_000572.1	Forward Primer	GGCGCTGTCATCGATTTCTT	SEQ ID NO: 1141
		Probe	CTGCTCCACGGCCTTGCTCTTG	SEQ ID NO: 1142
		Reverse Primer	TGGAGCTTATTAAAGGCATTCTTCA	SEQ ID NO: 1143

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
IL1B	NM_000576.2	Forward Primer	AGCTGAGGAAGATGCTGGTT	SEQ ID NO: 1144
		Probe	TGCCCACAGACCTTCCAGGAGAAT	SEQ ID NO: 1145
		Reverse Primer	GGAAAGAAGGTGCTCAGGTC	SEQ ID NO: 1146
IL6	NM_000600.1	Forward Primer	CCTGAACCTTCCAAAGATGG	SEQ ID NO: 1147
		Probe	CCAGATTGGAAGCATCCATCTTTTTCA	SEQ ID NO: 1148
		Reverse Primer	ACCAGGCAAGTCTCCTCATT	SEQ ID NO: 1149
IL6ST	NM_002184.2	Forward Primer	GGCCTAATGTTCCAGATCCT	SEQ ID NO: 1150
		Probe	CATATTGCCCAGTGGTCACCTCACA	SEQ ID NO: 1151
		Reverse Primer	AAAATTGTGCCTTGGAGGAG	SEQ ID NO: 1152
ILT-2	NM_006669.1	Forward Primer	AGCCATCACTCTCAGTGCAG	SEQ ID NO: 1153
		Probe	CAGGTCCTATCGTGGCCCCTGA	SEQ ID NO: 1154
		Reverse Primer	ACTGCAGAGTCAGGGTCTCC	SEQ ID NO: 1155
IMP-1	NM_006546.2	Forward Primer	GAAAGTGTTTGCGGAGCAC	SEQ ID NO: 1156
		Probe	CTCCTACAGCGGCCAGTTCTTGGT	SEQ ID NO: 1157
		Reverse Primer	GAAGGCGTAGCCGGATTT	SEQ ID NO: 1158
IMP2	NM_006548.3	Forward Primer	CAATCTGATCCCAGGGTTGAA	SEQ ID NO: 1159
		Probe	CTCAGCGCACTTGGCATCTTTTCAACA	SEQ ID NO: 1160
		Reverse Primer	GGCCCTGCTGGTGGAGATA	SEQ ID NO: 1161
ING1L	NM_001564.1	Forward Primer	TGTTTCCAAGATCCTGCTGA	SEQ ID NO: 1162
		Probe	CCATCTTTGCTTTATCTGAGGCTCGTTC	SEQ ID NO: 1163
		Reverse Primer	TCTTTCTGGTTGGCTGGAAT	SEQ ID NO: 1164
ING5	NM_032329.4	Forward Primer	CCTACAGCAAGTGCAAGGAA	SEQ ID NO: 1165
		Probe	CCAGCTGCACTTTGTCGTCACTGT	SEQ ID NO: 1166
		Reverse Primer	CATCTCGTAGGTCTGCATGG	SEQ ID NO: 1167
INHA	NM_002191.2	Forward Primer	CCTCCCAGTTTCATCTTCCACTA	SEQ ID NO: 1168
		Probe	ATGTGCAGCCCACAACCACCATGA	SEQ ID NO: 1169
		Reverse Primer	AGGGACTGGAAGGGACAGGTT	SEQ ID NO: 1170
INHBA	NM_002192.1	Forward Primer	GTGCCCGAGCCATATAGCA	SEQ ID NO: 1171
		Probe	ACGTCCGGGTCCTCACTGTCCTTCC	SEQ ID NO: 1172
		Reverse Primer	CGGTAGTGGTTGATGACTGTTGA	SEQ ID NO: 1173
INHBB	NM_002193.1	Forward Primer	AGCCTCCAGGATACCAGCAA	SEQ ID NO: 1174
		Probe	AGCTAAGCTGCCATTTGTCACCG	SEQ ID NO: 1175
		Reverse Primer	TCTCCGACTGACAGGCATTTG	SEQ ID NO: 1176
IRS1	NM_005544.1	Forward Primer	CCACAGCTCACCTTCTGTCA	SEQ ID NO: 1177
		Probe	TCCATCCCAGCTCCAGCCAG	SEQ ID NO: 1178
		Reverse Primer	CCTCAGTGCCAGTCTCTTCC	SEQ ID NO: 1179
ITGA3	NM_002204.1	Forward Primer	CCATGATCCTCACTCTGCTG	SEQ ID NO: 1180
		Probe	CACTCCAGACCTCGCTTAGCATGG	SEQ ID NO: 1181
		Reverse Primer	GAAGCTTTGTAGCCGGTGAT	SEQ ID NO: 1182
ITGA4	NM_000885.2	Forward Primer	CAACGCTTCAGTGATCAATCC	SEQ ID NO: 1183
		Probe	CGATCCTGCATCTGTAAATCGCCC	SEQ ID NO: 1184
		Reverse Primer	GTCTGGCCGGGATTCTTT	SEQ ID NO: 1185
ITGA5	NM_002205.1	Forward Primer	AGGCCAGCCCTACATTATCA	SEQ ID NO: 1186
		Probe	TCTGAGCCTTGTCCTCTATCCGGC	SEQ ID NO: 1187
		Reverse Primer	GTCTTCTCCACAGTCCAGCA	SEQ ID NO: 1188
ITGA6	NM_000210.1	Forward Primer	CAGTGACAAACAGCCCTTCC	SEQ ID NO: 1189
		Probe	TCGCCATCTTTTGTGGGATTCCTT	SEQ ID NO: 1190
		Reverse Primer	GTTTAGCCTCATGGGCGTC	SEQ ID NO: 1191
ITGA7	NM_002206.1	Forward Primer	GATATGATTGGTCGCTGCTTTG	SEQ ID NO: 1192
		Probe	CAGCCAGGACCTGGCCATCCG	SEQ ID NO: 1193
		Reverse Primer	AGAACTTCCATTCCCCACCAT	SEQ ID NO: 1194
ITGAV	NM_002210.2	Forward Primer	ACTCGGACTGCACAAGCTATT	SEQ ID NO: 1195
		Probe	CCGACAGCCACAGAATAACCCAAA	SEQ ID NO: 1196
		Reverse Primer	TGCCATCACCATTGAAATCT	SEQ ID NO: 1197
ITGB1	NM_002211.2	Forward Primer	TCAGAATTGGATTTGGCTCA	SEQ ID NO: 1198
		Probe	TGCTAATGTAAGGCATCACAGTCTTTTCCA	SEQ ID NO: 1199
		Reverse Primer	CCTGAGCTTAGCTGGTGTTG	SEQ ID NO: 1200

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
ITGB3	NM_000212.1	Forward Primer	ACCGGGAGCCCTACATGAC	SEQ ID NO: 1201
		Probe	AAATACCTGCAACCGTTACTGCCGTGAC	SEQ ID NO: 1202
		Reverse Primer	CCTTAAGCTCTTTCACTGACTCAATCT	SEQ ID NO: 1203
ITGB4	NM_000213.2	Forward Primer	CAAGGTGCCCTCAGTGGA	SEQ ID NO: 1204
		Probe	CACCAACCTGTACCCGTATTGCGA	SEQ ID NO: 1205
		Reverse Primer	GCGCACACCTTCATCTCAT	SEQ ID NO: 1206
ITGB5	NM_002213.3	Forward Primer	TCGTGAAAGATGACCAGGAG	SEQ ID NO: 1207
		Probe	TGCTATGTTTCTACAAAACCGCCAAGG	SEQ ID NO: 1208
		Reverse Primer	GGTGAACATCATGACGCAGT	SEQ ID NO: 1209
K-ras	NM_033360.2	Forward Primer	GTCAAAATGGGGAGGGACTA	SEQ ID NO: 1210
		Probe	TGTATCTTGTTGAGCTATCCAAACTGCCC	SEQ ID NO: 1211
		Reverse Primer	CAGGACCACCACAGAGTGAG	SEQ ID NO: 1212
KCNH2 iso a/b	NM_000238.2	Forward Primer	GAGCGCAAAGTGGAAATCG	SEQ ID NO: 1213
		Probe	TAGGAAGCAGCTCCCATCTTTCCGGTA	SEQ ID NO: 1214
		Reverse Primer	TCTTCACGGGCACCACATC	SEQ ID NO: 1215
KCNH2 iso a/c	NM_172057.1	Forward Primer	TCCTGCTGCTGGTCATCTAC	SEQ ID NO: 1216
		Probe	TGTCTTCACACCCTACTCGGCTGC	SEQ ID NO: 1217
		Reverse Primer	CCTTCTTCCGTCTCCTTCAG	SEQ ID NO: 1218
KCNK4	NM_016611.2	Forward Primer	CCTATCAGCCGCTGGTGT	SEQ ID NO: 1219
		Probe	ATCCTGCTCGGCCTGGCTTACTTC	SEQ ID NO: 1220
		Reverse Primer	TGGTGGTGAGCACTGAGG	SEQ ID NO: 1221
KDR	NM_002253.1	Forward Primer	GAGGACGAAGGCCTCTACAC	SEQ ID NO: 1222
		Probe	CAGGCATGCAGTGTTCTTGGCTGT	SEQ ID NO: 1223
		Reverse Primer	AAAAATGCCTCCACTTTTGC	SEQ ID NO: 1224
Ki-67	NM_002417.1	Forward Primer	CGGACTTTGGGTGCGACTT	SEQ ID NO: 1225
		Probe	CCACTTGTCGAACCACCGCTCGT	SEQ ID NO: 1226
		Reverse Primer	TTACAACTCTTCCACTGGGACGAT	SEQ ID NO: 1227
KIAA0125	NM_014792.2	Forward Primer	GTGTCCTGGTCCATGTGGT	SEQ ID NO: 1228
		Probe	CACGTGTCTCCACCTCCAAGGAGA	SEQ ID NO: 1229
		Reverse Primer	GGGAGGTGCACACTGAGG	SEQ ID NO: 1230
KIF22	NM_007317.1	Forward Primer	CTAAGGCACTTGCTGGAAGG	SEQ ID NO: 1231
		Probe	TCCATAGGCAAGCACACTGGCATT	SEQ ID NO: 1232
		Reverse Primer	TCTTCCCAGCTCCTGTGG	SEQ ID NO: 1233
KIF2C	NM_006845.2	Forward Primer	AATTCCTGCTCCAAAAGAAAGTCTT	SEQ ID NO: 1234
		Probe	AAGCCGCTCCACTCGCATGTCC	SEQ ID NO: 1235
		Reverse Primer	CGTGATGCGAAGCTCTGAGA	SEQ ID NO: 1236
KIFC1	XM_371813.1	Forward Primer	CCACAGGGTTGAAGAACCAG	SEQ ID NO: 1237
		Probe	AGCCAGTTCCTGCTGTTCCTGTCC	SEQ ID NO: 1238
		Reverse Primer	CACCTGATGTGCCAGACTTC	SEQ ID NO: 1239
Kitlng	NM_000899.1	Forward Primer	GTCCCCGGGATGGATGTT	SEQ ID NO: 1240
		Probe	CATCTCGCTTATCCAACAATGACTTGGCA	SEQ ID NO: 1241
		Reverse Primer	GATCAGTCAAGCTGTCTGACAATTG	SEQ ID NO: 1242
KLF5	NM_001730.3	Forward Primer	GTGCAACCGCAGCTTCTC	SEQ ID NO: 1243
		Probe	CTCTGACCACCTGGCCCTGCATAT	SEQ ID NO: 1244
		Reverse Primer	CGGGCAGTGCTCAGTTCT	SEQ ID NO: 1245
KLF6	NM_001300.4	Forward Primer	CACGAGACCGGCTACTTCTC	SEQ ID NO: 1246
		Probe	AGTACTCCTCCAGAGACGGCAGCG	SEQ ID NO: 1247
		Reverse Primer	GCTCTAGGCAGGTCTGTTGC	SEQ ID NO: 1248
KLK10	NM_002776.1	Forward Primer	GCCCAGAGGCTCCATCGT	SEQ ID NO: 1249
		Probe	CCTCTTCCTCCCCAGTCGGCTGA	SEQ ID NO: 1250
		Reverse Primer	CAGAGGTTTGAACAGTGCAGACA	SEQ ID NO: 1251
KLK6	NM_002774.2	Forward Primer	GACGTGAGGGTCCTGATTCT	SEQ ID NO: 1252
		Probe	TTACCCCAGCTCCATCCTTGCATC	SEQ ID NO: 1253
		Reverse Primer	TCCTCACTCATCACGTCCTC	SEQ ID NO: 1254
KLRK1	NM_007360.1	Forward Primer	TGAGAGCCAGGCTTCTTGTA	SEQ ID NO: 1255
		Probe	TGTCTCAAAATGCCAGCCTTCTGAA	SEQ ID NO: 1256
		Reverse Primer	ATCCTGGTCCTCTTTGCTGT	SEQ ID NO: 1257

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
KNTC2	NM_006101.1	Forward Primer	ATGTGCCAGTGAGCTTGAGT	SEQ ID NO: 1258
		Probe	CCTTGGAGAAACACAAGCACCTGC	SEQ ID NO: 1259
		Reverse Primer	TGAGCCCCTGGTTAACAGTA	SEQ ID NO: 1260
KRAS2	NM_004985.3	Forward Primer	GAGACCAAGGTTGCAAGGC	SEQ ID NO: 1261
		Probe	AAGCTCAAAGGTTCACACAGGGCC	SEQ ID NO: 1262
		Reverse Primer	CAGTCCATGCTGTGAAACTCTC	SEQ ID NO: 1263
KRT19	NM_002276.1	Forward Primer	TGAGCGGCAGAATCAGGAGTA	SEQ ID NO: 1264
		Probe	CTCATGGACATCAAGTCGCGGCTG	SEQ ID NO: 1265
		Reverse Primer	TGCGGTAGGTGGCAATCTC	SEQ ID NO: 1266
KRT8	NM_002273.1	Forward Primer	GGATGAAGCTTACATGAACAAGGTAGA	SEQ ID NO: 1267
		Probe	CGTCGGTCAGCCCTTCCAGGC	SEQ ID NO: 1268
		Reverse Primer	CATATAGCTGCCTGAGGAAGTTGAT	SEQ ID NO: 1269
LAMA3	NM_000227.2	Forward Primer	CAGATGAGGCACATGGAGAC	SEQ ID NO: 1270
		Probe	CTGATTCCTCAGGTCCTTGGCCTG	SEQ ID NO: 1271
		Reverse Primer	TTGAAATGGCAGAACGGTAG	SEQ ID NO: 1272
LAMB3	NM_000228.1	Forward Primer	ACTGACCAAGCCTGAGACCT	SEQ ID NO: 1273
		Probe	CCACTCGCCATACTGGGTGCAGT	SEQ ID NO: 1274
		Reverse Primer	GTCACACTTGCAGCATTTCA	SEQ ID NO: 1275
LAMC2	NM_005562.1	Forward Primer	ACTCAAGCGGAAATTGAAGCA	SEQ ID NO: 1276
		Probe	AGGTCTTATCAGCACAGTCTCCGCCTCC	SEQ ID NO: 1277
		Reverse Primer	ACTCCCTGAAGCCGAGACACT	SEQ ID NO: 1278
LAT	NM_014387.2	Forward Primer	GTGAACGTTCCGGAGAGC	SEQ ID NO: 1279
		Probe	ATCCAGAGACGCTTCTGCGCTCTC	SEQ ID NO: 1280
		Reverse Primer	ACATTCACATACTCCCGGCT	SEQ ID NO: 1281
LCN2	NM_005564.2	Forward Primer	CGCTGGGCAACATTAAGAG	SEQ ID NO: 1282
		Probe	TCACCACTCGGACGAGGTAACTCG	SEQ ID NO: 1283
		Reverse Primer	AGCATGCTGGTTGTAGTTGGT	SEQ ID NO: 1284
LDLRAP1	NM_015627.1	Forward Primer	CAGTGCCTCTCGCCTGTC	SEQ ID NO: 1285
		Probe	ACTGGGACAAGCCTGACAGCAGC	SEQ ID NO: 1286
		Reverse Primer	TGAAGAGGTCATCCTGCTCTG	SEQ ID NO: 1287
LEF	NM_016269.2	Forward Primer	GATGACGGAAAGCATCCAG	SEQ ID NO: 1288
		Probe	TGGAGGCCTCTACAACAAGGGACC	SEQ ID NO: 1289
		Reverse Primer	CCCGGAATAACTCGAGTAGGA	SEQ ID NO: 1290
LGALS3	NM_002306.1	Forward Primer	AGCGGAAAATGGCAGACAAT	SEQ ID NO: 1291
		Probe	ACCCAGATAACGCATCATGGAGCGA	SEQ ID NO: 1292
		Reverse Primer	CTTGAGGGTTTGGGTTTCCA	SEQ ID NO: 1293
LGMN	NM_001008530.1	Forward Primer	TTGGTGCCGTTCCTATAGATG	SEQ ID NO: 1294
		Probe	CAGTGCTTGCCTCCATCTTCAGGA	SEQ ID NO: 1295
		Reverse Primer	GAACCTGCCACGATCACC	SEQ ID NO: 1296
LILRB3	NM_006864.1	Forward Primer	CACCTGGTCTGGGAAGATACC	SEQ ID NO: 1297
		Probe	ACCGAGACCCCAATCAAAACCTCC	SEQ ID NO: 1298
		Reverse Primer	AAGAGCAGCAGGACGAAGG	SEQ ID NO: 1299
LMNB1	NM_005573.1	Forward Primer	TGCAAACGCTGGTGTCACA	SEQ ID NO: 1300
		Probe	CAGCCCCCCAACTGACCTCATC	SEQ ID NO: 1301
		Reverse Primer	CCCCACGAGTTCTGGTTCTTC	SEQ ID NO: 1302
LMYC	NM_012421.1	Forward Primer	CCCATCCAGAACACTGATTG	SEQ ID NO: 1303
		Probe	TGACCTCCATCCCTTTCACTTGAATG	SEQ ID NO: 1304
		Reverse Primer	CTGCTTTCTATGCACCCTTTC	SEQ ID NO: 1305
LOX	NM_002317.3	Forward Primer	CCAATGGGAGAACAACGG	SEQ ID NO: 1306
		Probe	CAGGCTCAGCAAGCTGAACACCTG	SEQ ID NO: 1307
		Reverse Primer	CGCTGAGGCTGGTACTGTG	SEQ ID NO: 1308
LOXL2	NM_002318.1	Forward Primer	TCAGCGGGCTCTTAAACAA	SEQ ID NO: 1309
		Probe	CAGCTGTCCCCGCAGTAAAGAAGC	SEQ ID NO: 1310
		Reverse Primer	AAGACAGGAGTTGACCACGC	SEQ ID NO: 1311
LRP5	NM_002335.1	Forward Primer	CGACTATGACCCACTGGACA	SEQ ID NO: 1312
		Probe	CGCCCATCCACCCAGTAGATGAAC	SEQ ID NO: 1313
		Reverse Primer	CTTGGCTCGCTTGATGTTC	SEQ ID NO: 1314

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
LRP6	NM_002336.1	Forward Primer	GGATGTAGCCATCTCTGCCT	SEQ ID NO: 1315
		Probe	ATAGACCTCAGGGCCTTCGCTGTG	SEQ ID NO: 1316
		Reverse Primer	AGTTCAAAGCCAATAGGGCA	SEQ ID NO: 1317
LY6D	NM_003695.2	Forward Primer	AATGCTGATGACTTGGAGCAG	SEQ ID NO: 1318
		Probe	CACAGACCCCACAGAGGATGAAGC	SEQ ID NO: 1319
		Reverse Primer	CTGCATCCTCTGTGGGGT	SEQ ID NO: 1320
MAD	NM_002357.1	Forward Primer	TGGTTCTGATTAGGTAACGTATTGGA	SEQ ID NO: 1321
		Probe	CTGCCCACAACTCCCTTGCACGTAA	SEQ ID NO: 1322
		Reverse Primer	GGTCAAGGTGGGACACTGAAG	SEQ ID NO: 1323
MAD1L1	NM_003550.1	Forward Primer	AGAAGCTGTCCCTGCAAGAG	SEQ ID NO: 1324
		Probe	CATGTTCTTCACAATCGCTGCATCC	SEQ ID NO: 1325
		Reverse Primer	AGCCGTACCAGCTCAGACTT	SEQ ID NO: 1326
MAD2L1	NM_002358.2	Forward Primer	CCGGGAGCAGGGAATCAC	SEQ ID NO: 1327
		Probe	CGGCCACGATTTCGGCGCT	SEQ ID NO: 1328
		Reverse Primer	ATGCTGTTGATGCCGAATGA	SEQ ID NO: 1329
MADH2	NM_005901.2	Forward Primer	GCTGCCTTTGGTAAGAACATGTC	SEQ ID NO: 1330
		Probe	TCCATCTTGCCATTCACGCCGC	SEQ ID NO: 1331
		Reverse Primer	ATCCCAGCAGTCTCTTCACAACT	SEQ ID NO: 1332
MADH4	NM_005359.3	Forward Primer	GGACATTACTGGCCTGTTCACA	SEQ ID NO: 1333
		Probe	TGCATTCCAGCCTCCCATTTCCA	SEQ ID NO: 1334
		Reverse Primer	ACCAATACTCAGGAGCAGGATGA	SEQ ID NO: 1335
MADH7	NM_005904.1	Forward Primer	TCCATCAAGGCTTTCGACTA	SEQ ID NO: 1336
		Probe	CTGCAGGCTGTACGCCTTCTCG	SEQ ID NO: 1337
		Reverse Primer	CTGCTGCATAAACTCGTGGT	SEQ ID NO: 1338
MAP2	NM_031846.1	Forward Primer	CGGACCACCAGGTCAGAG	SEQ ID NO: 1339
		Probe	CCACTCTTCCCTGCTCTGCGAATT	SEQ ID NO: 1340
		Reverse Primer	CAGGGGTAGTGGGTGTTGAG	SEQ ID NO: 1341
MAP2K1	NM_002755.2	Forward Primer	GCCTTTCTTACCCAGAAGCAGAA	SEQ ID NO: 1342
		Probe	TCTCAAAGTCGTCATCCTTCAGTTCTCCCA	SEQ ID NO: 1343
		Reverse Primer	CAGCCCCCAGCTCACTGAT	SEQ ID NO: 1344
MAP3K1	XM_042066.8	Forward Primer	GGTTGGCATCAAAAGGAACT	SEQ ID NO: 1345
		Probe	AATTGTCCCTGAAACTCTCCTGCACC	SEQ ID NO: 1346
		Reverse Primer	TGCCATAAATGCAATTGTCC	SEQ ID NO: 1347
MAPK14	NM_139012.1	Forward Primer	TGAGTGGAAAAGCCTGACCTATG	SEQ ID NO: 1348
		Probe	TGAAGTCATCAGCTTTGTGCCACCACC	SEQ ID NO: 1349
		Reverse Primer	GGACTCCATCTCTTCTTGGTCAA	SEQ ID NO: 1350
Maspin	NM_002639.1	Forward Primer	CAGATGGCCACTTTGAGAACATT	SEQ ID NO: 1351
		Probe	AGCTGACAACAGTGTGAACGACCAGACC	SEQ ID NO: 1352
		Reverse Primer	GGCAGCATTAACCACAAGGATT	SEQ ID NO: 1353
MAX	NM_002382.3	Forward Primer	CAAACGGGCTCATCATAATGC	SEQ ID NO: 1354
		Probe	TGATGTGGTCCCTACGTTTTCGTTCCA	SEQ ID NO: 1355
		Reverse Primer	TCCCGCAAACTGTGAAAGCT	SEQ ID NO: 1356
MCM2	NM_004526.1	Forward Primer	GACTTTTGCCCGCTACCTTTC	SEQ ID NO: 1357
		Probe	ACAGCTCATTGTTGTCACGCCGGA	SEQ ID NO: 1358
		Reverse Primer	GCCACTAACTGCTTCAGTATGAAGAG	SEQ ID NO: 1359
MCM3	NM_002388.2	Forward Primer	GGAGAACAATCCCCTTGAGA	SEQ ID NO: 1360
		Probe	TGGCCTTTCTGTCTACAAGGATCACCA	SEQ ID NO: 1361
		Reverse Primer	ATCTCCTGGATGGTGATGGT	SEQ ID NO: 1362
MCM6	NM_005915.2	Forward Primer	TGATGGTCCTATGTGTCACATTCA	SEQ ID NO: 1363
		Probe	CAGGTTTCATACCAACACAGGCTTCAGCAC	SEQ ID NO: 1364
		Reverse Primer	TGGGACAGGAAACACACCAA	SEQ ID NO: 1365
MCP1	NM_002982.1	Forward Primer	CGCTCAGCCAGATGCAATC	SEQ ID NO: 1366
		Probe	TGCCCCAGTCACCTGCTGTTA	SEQ ID NO: 1367
		Reverse Primer	GCACTGAGATCTTCCTATTGGTGAA	SEQ ID NO: 1368
MDK	NM_002391.2	Forward Primer	GGAGCCGACTGCAAGTACA	SEQ ID NO: 1369
		Probe	ATCACACGCACCCCAGTTCTCAAA	SEQ ID NO: 1370
		Reverse Primer	GACTTTGGTGCCTGTGCC	SEQ ID NO: 1371

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
MDM2	NM_002392.1	Forward Primer	CTACAGGGACGCCATCGAA	SEQ ID NO: 1372
		Probe	CTTACACCAGCATCAAGATCCGG	SEQ ID NO: 1373
		Reverse Primer	ATCCAACCAATCACCTGAATGTT	SEQ ID NO: 1374
MGAT5	NM_002410.2	Forward Primer	GGAGTCGAAGGTGGACAATC	SEQ ID NO: 1375
		Probe	AATGGCACCGGAACAAACTCAACC	SEQ ID NO: 1376
		Reverse Primer	TGGGAACAGCTGTAGTGGAGT	SEQ ID NO: 1377
MGMT	NM_002412.1	Forward Primer	GTGAAATGAAACGCACCACA	SEQ ID NO: 1378
		Probe	CAGCCCTTTGGGGAAGCTGG	SEQ ID NO: 1379
		Reverse Primer	GACCCTGCTCACAACCAGAC	SEQ ID NO: 1380
mGST1	NM_020300.2	Forward Primer	ACGGATCTACCACACCATTGC	SEQ ID NO: 1381
		Probe	TTTGACACCCCTTCCCCAGCCA	SEQ ID NO: 1382
		Reverse Primer	TCCATATCCAACAAAAAAACTCAAAG	SEQ ID NO: 1383
MMP1	NM_002421.2	Forward Primer	GGGAGATCATCGGGACAACTC	SEQ ID NO: 1384
		Probe	AGCAAGATTTCCTCCAGGTCCATCAAAAGG	SEQ ID NO: 1385
		Reverse Primer	GGGCCTGGTTGAAAAGCAT	SEQ ID NO: 1386
MMP12	NM_002426.1	Forward Primer	CCAACGCTTGCCAAATCCT	SEQ ID NO: 1387
		Probe	AACCAGCTCTCTGTGACCCCAATT	SEQ ID NO: 1388
		Reverse Primer	ACGGTAGTGACAGCATCAAAACTC	SEQ ID NO: 1389
MMP2	NM_004530.1	Forward Primer	CCATGATGGAGAGGCAGACA	SEQ ID NO: 1390
		Probe	CTGGGAGCATGGCGATGGATACCC	SEQ ID NO: 1391
		Reverse Primer	GGAGTCCGTCCTTACCGTCAA	SEQ ID NO: 1392
MMP7	NM_002423.2	Forward Primer	GGATGGTAGCAGTCTAGGGATTAACT	SEQ ID NO: 1393
		Probe	CCTGTATGCTGCAACTCATGAACTTGGC	SEQ ID NO: 1394
		Reverse Primer	GGAATGTCCCATACCCAAAGAA	SEQ ID NO: 1395
MMP9	NM_004994.1	Forward Primer	GAGAACCAATCTCACCGACA	SEQ ID NO: 1396
		Probe	ACAGGTATTCCTCTGCCAGCTGCC	SEQ ID NO: 1397
		Reverse Primer	CACCCGAGTGTAACCATAGC	SEQ ID NO: 1398
MRP1	NM_004996.2	Forward Primer	TCATGGTGCCCGTCAATG	SEQ ID NO: 1399
		Probe	ACCTGATACGTCTTGGTCTTCATCGCCAT	SEQ ID NO: 1400
		Reverse Primer	CGATTGTCTTTGCTCTTCATGTG	SEQ ID NO: 1401
MRP2	NM_000392.1	Forward Primer	AGGGGATGACTTGGACACAT	SEQ ID NO: 1402
		Probe	CTGCCATTCGACATGACTGCAATTT	SEQ ID NO: 1403
		Reverse Primer	AAAACTGCATGGCTTTGTCA	SEQ ID NO: 1404
MRP3	NM_003786.2	Forward Primer	TCATCCTGGCGATCTACTTCCT	SEQ ID NO: 1405
		Probe	TCTGTCCTGGCTGGAGTCGCTTTCAT	SEQ ID NO: 1406
		Reverse Primer	CCGTTGAGTGGAATCAGCAA	SEQ ID NO: 1407
MRP4	NM_005845.1	Forward Primer	AGCGCCTGGAATCTACAACT	SEQ ID NO: 1408
		Probe	CGGAGTCCAGTGTTTTCCCACTTG	SEQ ID NO: 1409
		Reverse Primer	AGAGCCCCTGGAGAGAAGAT	SEQ ID NO: 1410
MRPL40	NM_003776.2	Forward Primer	ACTTGCAGGCTGCTATCCTT	SEQ ID NO: 1411
		Probe	TTCCTACTCTCAGGGGCAGCATGTT	SEQ ID NO: 1412
		Reverse Primer	AGCAGACTTGAACCCTGGTC	SEQ ID NO: 1413
MSH2	NM_000251.1	Forward Primer	GATGCAGAATTGAGGCAGAC	SEQ ID NO: 1414
		Probe	CAAGAAGATTTACTTCGTCGATTCCCAGA	SEQ ID NO: 1415
		Reverse Primer	TCTTGGCAAGTCGGTTAAGA	SEQ ID NO: 1416
MSH3	NM_002439.1	Forward Primer	TGATTACCATCATGGCTCAGA	SEQ ID NO: 1417
		Probe	TCCCAATTGTCGCTTCTTCTGCAG	SEQ ID NO: 1418
		Reverse Primer	CTTGTGAAAATGCCATCCAC	SEQ ID NO: 1419
MSH6	NM_000179.1	Forward Primer	TCTATTGGGGGATTGGTAGG	SEQ ID NO: 1420
		Probe	CCGTTACCAGCTGGAAATTCCTGAGA	SEQ ID NO: 1421
		Reverse Primer	CAAATTGCGAGTGGTGAAAT	SEQ ID NO: 1422
MT3	NM_005954.1	Forward Primer	GTGTGAGAAGTGTGCCAAGG	SEQ ID NO: 1423
		Probe	CTCTCCGCCTTTGCACACACAGT	SEQ ID NO: 1424
		Reverse Primer	CTGCACTTCTCTGCTTCTGC	SEQ ID NO: 1425
MTA1	NM_004689.2	Forward Primer	CCGCCCTCACCTGAAGAGA	SEQ ID NO: 1426
		Probe	CCCAGTGTCCGCCAAGGAGCG	SEQ ID NO: 1427
		Reverse Primer	GGAATAAGTTAGCCGCGCTTCT	SEQ ID NO: 1428

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
MUC1	NM_002456.1	Forward Primer	GGCCAGGATCTGTGGTGGTA	SEQ ID NO: 1429
		Probe	CTCTGGCCTTCCGAGAAGGTACC	SEQ ID NO: 1430
		Reverse Primer	CTCCACGTCGTGGACATTGA	SEQ ID NO: 1431
MUC2	NM_002457.1	Forward Primer	CTATGAGCCATGTGGGAACC	SEQ ID NO: 1432
		Probe	AGCTTCGAGACCTGCAGGACCATC	SEQ ID NO: 1433
		Reverse Primer	ATGTTGGAGTGGATGCCG	SEQ ID NO: 1434
MUC5B	XM_039877.11	Forward Primer	TGCCCTTGCACTGTCCTAA	SEQ ID NO: 1435
		Probe	TCAGCCATCCTGCACACCTACACC	SEQ ID NO: 1436
		Reverse Primer	CAGCCACACTCATCCACG	SEQ ID NO: 1437
MUTYH	NM_012222.1	Forward Primer	GTACGACCAAGAGAAACGGG	SEQ ID NO: 1438
		Probe	TCTGCCCGTCTTCTCCATGGTAGG	SEQ ID NO: 1439
		Reverse Primer	CCTGTCCAGGTCCATCTCA	SEQ ID NO: 1440
MVP	NM_017458.1	Forward Primer	ACGAGAACGAGGGCATCTATGT	SEQ ID NO: 1441
		Probe	CGCACCTTTCCGGTCTTGACATCCT	SEQ ID NO: 1442
		Reverse Primer	GCATGTAGGTGCTTCCAATCAC	SEQ ID NO: 1443
MX1	NM_002462.2	Forward Primer	GAAGGAATGGGAATCAGTCATGA	SEQ ID NO: 1444
		Probe	TCACCCTGGAGATCAGCTCCCGA	SEQ ID NO: 1445
		Reverse Primer	GTCTATTAGAGTCAGATCCGGGACAT	SEQ ID NO: 1446
MXD4	NM_006454.2	Forward Primer	AGAAACTGGAGGAGCAGGAC	SEQ ID NO: 1447
		Probe	TGCAGCTGCTCCTTGATGCTCAGT	SEQ ID NO: 1448
		Reverse Primer	CTTCAGGAAACGATGCTCCT	SEQ ID NO: 1449
MYBL2	NM_002466.1	Forward Primer	GCCGAGATCGCCAAGATG	SEQ ID NO: 1450
		Probe	CAGCATTGTCTGTCCTCCCTGGCA	SEQ ID NO: 1451
		Reverse Primer	CTTTTGATGGTAGAGTTCCAGTGATTC	SEQ ID NO: 1452
MYH11	NM_002474.1	Forward Primer	CGGTACTTCTCAGGGCTAATATATACG	SEQ ID NO: 1453
		Probe	CTCTTCTGCGTGGTGGTCAACCCCTA	SEQ ID NO: 1454
		Reverse Primer	CCGAGTAGATGGGCAGGTGTT	SEQ ID NO: 1455
MYLK	NM_053025.1	Forward Primer	TGACGGAGCGTGAGTGCAT	SEQ ID NO: 1456
		Probe	CCCTCCGAGATCTGCCGCATGTACT	SEQ ID NO: 1457
		Reverse Primer	ATGCCCTGCTTGTGGATGTAC	SEQ ID NO: 1458
NAT2	NM_000015.1	Forward Primer	TAACTGACATTCTTGAGCACCAGAT	SEQ ID NO: 1459
		Probe	CGGGCTGTTCCCTTTGAGAACCTTAACA	SEQ ID NO: 1460
		Reverse Primer	ATGGCTTGCCCACAATGC	SEQ ID NO: 1461
NAV2	NM_182964.3	Forward Primer	CTCTCCCAGCACAGCTTGA	SEQ ID NO: 1462
		Probe	CCTCACTGAGTCAACCAGCCTGGA	SEQ ID NO: 1463
		Reverse Primer	CACCAGTGTCATCCAGCAAC	SEQ ID NO: 1464
NCAM1	NM_000615.1	Forward Primer	TAGTTCCCAGCTGACCATCA	SEQ ID NO: 1465
		Probe	CTCAGCCTCGTCGTTCTTATCCACC	SEQ ID NO: 1466
		Reverse Primer	CAGCCTTGTTCTCAGCAATG	SEQ ID NO: 1467
NDE1	NM_017668.1	Forward Primer	CTACTGCGGAAAGTCGGG	SEQ ID NO: 1468
		Probe	CTGGAGTCCAAACTCGCTTCCTGC	SEQ ID NO: 1469
		Reverse Primer	GGACTGATCGTACACGAGGTT	SEQ ID NO: 1470
NDRG1	NM_006096.2	Forward Primer	AGGGCAACATTCCACAGC	SEQ ID NO: 1471
		Probe	CTGCAAGGACACTCATCACAGCCA	SEQ ID NO: 1472
		Reverse Primer	CAGTGCTCCTACTCCGGC	SEQ ID NO: 1473
NDUFS3	NM_004551.1	Forward Primer	TATCCATCCTGATGGCGTC	SEQ ID NO: 1474
		Probe	CCCAGTGCTGACTTTCCTCAGGGA	SEQ ID NO: 1475
		Reverse Primer	TTGAACTGTGCATTGGTGTG	SEQ ID NO: 1476
NEDD8	NM_006156.1	Forward Primer	TGCTGGCTACTGGGTGTTAGT	SEQ ID NO: 1477
		Probe	TGCAGTCCTGTGTGCTTCCCTCTC	SEQ ID NO: 1478
		Reverse Primer	GACAACCAGGGACACAGTCA	SEQ ID NO: 1479
NEK2	NM_002497.1	Forward Primer	GTGAGGCAGCGCGACTCT	SEQ ID NO: 1480
		Probe	TGCCTTCCCGGGCTGAGGACT	SEQ ID NO: 1481
		Reverse Primer	TGCCAATGGTGTACAACACTTCA	SEQ ID NO: 1482
NF2	NM_000268.2	Forward Primer	ACTCCAGAGCTGACCTCCAC	SEQ ID NO: 1483
		Probe	CTACAATGACTTCCCAGGCTGGGC	SEQ ID NO: 1484
		Reverse Primer	TCAGGGCTTCAGTGTCTCAC	SEQ ID NO: 1485

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
NFKBp50	NM_003998.1	Forward Primer	CAGACCAAGGAGATGGACCT	SEQ ID NO: 1486
		Probe	AAGCTGTAAACATGAGCCGCACCA	SEQ ID NO: 1487
		Reverse Primer	AGCTGCCAGTGCTATCCG	SEQ ID NO: 1488
NFKBp65	NM_021975.1	Forward Primer	CTGCCGGGATGGCTTCTAT	SEQ ID NO: 1489
		Probe	CTGAGCTCTGCCCGGACCGCT	SEQ ID NO: 1490
		Reverse Primer	CCAGGTTCTGGAAACTGTGGAT	SEQ ID NO: 1491
NISCH	NM_007184.1	Forward Primer	CCAAGGAATCATGTTCGTTCAG	SEQ ID NO: 1492
		Probe	TGGCCAGCAGCCTCTCGTCCAC	SEQ ID NO: 1493
		Reverse Primer	TGGTGCTCGGGAGTCAGACT	SEQ ID NO: 1494
Nkd-1	NM_033119.3	Forward Primer	GAGAGAGTGAGCGAACCCTG	SEQ ID NO: 1495
		Probe	CCAGGCTCCAAGAAGCAGCTGAAG	SEQ ID NO: 1496
		Reverse Primer	CGTCGCACTGGAGCTCTT	SEQ ID NO: 1497
NMB	NM_021077.1	Forward Primer	GGCTGCTGGTACAAATACTGC	SEQ ID NO: 1498
		Probe	TGTCTGCCCCTATTATTGGTGTCATTTCT	SEQ ID NO: 1499
		Reverse Primer	CAATCTAAGCCACGCTGTTG	SEQ ID NO: 1500
NMBR	NM_002511.1	Forward Primer	TGATCCATCTCTAGGCCACA	SEQ ID NO: 1501
		Probe	TTGTCACCTTAGTTGCCCGGGTTC	SEQ ID NO: 1502
		Reverse Primer	GAGCAAATGGGTTGACACAA	SEQ ID NO: 1503
NME1	NM_000269.1	Forward Primer	CCAACCCTGCAGACTCCAA	SEQ ID NO: 1504
		Probe	CCTGGGACCATCCGTGGAGACTTCT	SEQ ID NO: 1505
		Reverse Primer	ATGTATAATGTTCCTGCCAACTTGTATG	SEQ ID NO: 1506
NOS3	NM_000603.2	Forward Primer	ATCTCCGCCTCGCTCATG	SEQ ID NO: 1507
		Probe	TTCACTCGCTTCGCCATCACCG	SEQ ID NO: 1508
		Reverse Primer	TCGGAGCCATACAGGATTGTC	SEQ ID NO: 1509
NOTCH1	NM_017617.2	Forward Primer	CGGGTCCACCAGTTTGAATG	SEQ ID NO: 1510
		Probe	CCGCTCTGCAGCCGGGACA	SEQ ID NO: 1511
		Reverse Primer	GTTGTATTGGTTCGGCACCAT	SEQ ID NO: 1512
NOTCH2	NM_024408.2	Forward Primer	CACTTCCCTGCTGGGATTAT	SEQ ID NO: 1513
		Probe	CCGTGTTGCACAGCTCATCACACT	SEQ ID NO: 1514
		Reverse Primer	AGTTGTCAAACAGGCACTCG	SEQ ID NO: 1515
NPM1	NM_002520.2	Forward Primer	AATGTTGTCCAGGTTCTATTGC	SEQ ID NO: 1516
		Probe	AACAGGCATTTTGGACAACACATTCTTG	SEQ ID NO: 1517
		Reverse Primer	CAAGCAAAGGGTGGAGTTC	SEQ ID NO: 1518
NR4A1	NM_002135.2	Forward Primer	CACAGCTTGCTTGTCGATGTC	SEQ ID NO: 1519
		Probe	CCTTCGCCTGCCTCTCTGCCC	SEQ ID NO: 1520
		Reverse Primer	ATGCCGGTCGGTGATGAG	SEQ ID NO: 1521
NRG1	NM_013957.1	Forward Primer	CGAGACTCTCCTCATAGTGAAAGGTAT	SEQ ID NO: 1522
		Probe	ATGACCACCCCGGCTCGTATGTCA	SEQ ID NO: 1523
		Reverse Primer	CTTGGCGTGTGGAAATCTACAG	SEQ ID NO: 1524
NRP1	NM_003873.1	Forward Primer	CAGCTCTCTCCACGCGATTC	SEQ ID NO: 1525
		Probe	CAGGATCTACCCCGAGAGAGCCACTCAT	SEQ ID NO: 1526
		Reverse Primer	CCCAGCAGCTCCATTCTGA	SEQ ID NO: 1527
NRP2	NM_003872.1	Forward Primer	CTACAGCCTAAACGGCAAGG	SEQ ID NO: 1528
		Probe	AGGACCCCAGGACCCAGCAG	SEQ ID NO: 1529
		Reverse Primer	GTTCCCTTCGAACAGCTTTG	SEQ ID NO: 1530
NTN1	NM_004822.1	Forward Primer	AGAAGGACTATGCCGTCCAG	SEQ ID NO: 1531
		Probe	ATCCACATCCTGAAGGCGGACAAG	SEQ ID NO: 1532
		Reverse Primer	CCGTGAACTTCCACCAGTC	SEQ ID NO: 1533
NUFIP1	NM_012345.1	Forward Primer	GCTTCCACATCGTGGTATTG	SEQ ID NO: 1534
		Probe	CTTCTGATAGGTTTCCTCGGCATCAGA	SEQ ID NO: 1535
		Reverse Primer	AACTGCAGGGTTGAAGGACT	SEQ ID NO: 1536
ODC1	NM_002539.1	Forward Primer	AGAGATCACCGGCGTAATCAA	SEQ ID NO: 1537
		Probe	CCAGCGTTGGACAAATACTTTCCGTCA	SEQ ID NO: 1538
		Reverse Primer	CGGGCTCAGCTATGATTCTCA	SEQ ID NO: 1539

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
OPN, osteopontin	NM_000582.1	Forward Primer	CAACCGAAGTTTTCACTCCAGTT	SEQ ID NO: 1540
		Probe	TCCCCACAGTAGACACATATGATGGCCG	SEQ ID NO: 1541
		Reverse Primer	CCTCAGTCCATAAACCACACTATCA	SEQ ID NO: 1542
ORC1L	NM_004153.2	Forward Primer	TCCTTGACCATACCGGAGG	SEQ ID NO: 1543
		Probe	TGCATGTACATCTCCGGTGTCCCT	SEQ ID NO: 1544
		Reverse Primer	CAGTGGCAGTCTTCCCTGTC	SEQ ID NO: 1545
OSM	NM_020530.3	Forward Primer	GTTTCTGAAGGGGAGGTCAC	SEQ ID NO: 1546
		Probe	CTGAGCTGGCCTCCTATGCCTCAT	SEQ ID NO: 1547
		Reverse Primer	AGGTGTCTGGTTTGGGACA	SEQ ID NO: 1548
OSMR	NM_003999.1	Forward Primer	GCTCATCATGGTCATGTGCT	SEQ ID NO: 1549
		Probe	CAGGTCTCCTTGATCCACTGACTTTTCA	SEQ ID NO: 1550
		Reverse Primer	TGTAAGGGTCAGGGATGTCA	SEQ ID NO: 1551
P14ARF	S78535.1	Forward Primer	CCCTCGTGCTGATGCTACT	SEQ ID NO: 1552
		Probe	CTGCCCTAGACGCTGGCTCCTC	SEQ ID NO: 1553
		Reverse Primer	CATCATGACCTGGTCTTCTAGG	SEQ ID NO: 1554
p16-INK4	L27211.1	Forward Primer	GCGGAAGGTCCCTCAGACA	SEQ ID NO: 1555
		Probe	CTCAGAGCCTCTCTGGTTCTTTCAATCGG	SEQ ID NO: 1556
		Reverse Primer	TGATGATCTAAGTTTCCCGAGGTT	SEQ ID NO: 1557
p21	NM_000389.1	Forward Primer	TGGAGACTCTCAGGGTCGAAA	SEQ ID NO: 1558
		Probe	CGGCGGCAGACCAGCATGAC	SEQ ID NO: 1559
		Reverse Primer	GGCGTTTGGAGTGGTAGAAATC	SEQ ID NO: 1560
p27	NM_004064.1	Forward Primer	CGGTGGACCACGAAGAGTTAA	SEQ ID NO: 1561
		Probe	CCGGGACTTGGAGAAGCACTGCA	SEQ ID NO: 1562
		Reverse Primer	GGCTCGCCTCTTCCATGTC	SEQ ID NO: 1563
P53	NM_000546.2	Forward Primer	CTTTGAACCCTTGCTTGCAA	SEQ ID NO: 1564
		Probe	AAGTCCTGGGTGCTTCTGACGCACA	SEQ ID NO: 1565
		Reverse Primer	CCCGGGACAAAGCAAATG	SEQ ID NO: 1566
p53R2	AB036063.1	Forward Primer	CCCAGCTAGTGTTCCTCAGA	SEQ ID NO: 1567
		Probe	TCGGCCAGCTTTTTCCAATCTTTG	SEQ ID NO: 1568
		Reverse Primer	CCGTAAGCCCTTCCTCTATG	SEQ ID NO: 1569
PADI4	NM_012387.1	Forward Primer	AGCAGTGGCTTGCTTTCTTC	SEQ ID NO: 1570
		Probe	CCTGTGATGTCCCAGTTTCCCACTC	SEQ ID NO: 1571
		Reverse Primer	TGCTAGGACCATGTTGGGAT	SEQ ID NO: 1572
PAI1	NM_000602.1	Forward Primer	CCGCAACGTGGTTTTCTCA	SEQ ID NO: 1573
		Probe	CTCGGTGTTGGCCATGCTCCAG	SEQ ID NO: 1574
		Reverse Primer	TGCTGGGTTTCTCCTCCTGTT	SEQ ID NO: 1575
Pak1	NM_002576.3	Forward Primer	GAGCTGTGGGTTGTTATGGA	SEQ ID NO: 1576
		Probe	ACATCTGTCAAGGAGCCTCCAGCC	SEQ ID NO: 1577
		Reverse Primer	CCATGCAAGTTTCTGTCACC	SEQ ID NO: 1578
PARC	NM_015089.1	Forward Primer	GGAGCTGACCTGCTTCCTAC	SEQ ID NO: 1579
		Probe	TCCTTATGCATCGAGGCCAGGC	SEQ ID NO: 1580
		Reverse Primer	AGCAGAGCACCACAGCATAG	SEQ ID NO: 1581
PCAF	NM_003884.3	Forward Primer	AGGTGGCTGTGTTACTGCAA	SEQ ID NO: 1582
		Probe	TGCCACAGTTCTGCGACAGTCTACC	SEQ ID NO: 1583
		Reverse Primer	CACCTGTGTGGTTTCGTACC	SEQ ID NO: 1584
PCNA	NM_002592.1	Forward Primer	GAAGGTGTTGGAGGCACTCAAG	SEQ ID NO: 1585
		Probe	ATCCCAGCAGGCCTCGTTGATGAG	SEQ ID NO: 1586
		Reverse Primer	GGTTTACACCGCTGGAGCTAA	SEQ ID NO: 1587
PDGFA	NM_002607.2	Forward Primer	TTGTTGGTGTGCCCTGGTG	SEQ ID NO: 1588
		Probe	TGGTGGCGGTCACTCCCTCTGC	SEQ ID NO: 1589
		Reverse Primer	TGGGTTCTGTCCAAACACTGG	SEQ ID NO: 1590
PDGFB	NM_002608.1	Forward Primer	ACTGAAGGAGACCCTTGGAG	SEQ ID NO: 1591
		Probe	TCTCCTGCCGATGCCCCTAGG	SEQ ID NO: 1592
		Reverse Primer	TAAATAACCCTGCCCACACA	SEQ ID NO: 1593

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
PDGFC	NM_016205.1	Forward Primer	AGTTACTAAAAAATACCACGAGGTCCTT	SEQ ID NO: 1594
		Probe	CCCTGACACCGGTCTTTGGTCTCAACT	SEQ ID NO: 1595
		Reverse Primer	GTCGGTGAGTGATTTGTGCAA	SEQ ID NO: 1596
PDGFD	NM_025208.2	Forward Primer	TATCGAGGCAGGTCATACCA	SEQ ID NO: 1597
		Probe	TCCAGGTCAACTTTTGACTTCCGGT	SEQ ID NO: 1598
		Reverse Primer	TAACGCTTGGCATCATCATT	SEQ ID NO: 1599
PDGFRa	NM_006206.2	Forward Primer	GGGAGTTTCCAAGAGATGGA	SEQ ID NO: 1600
		Probe	CCCAAGACCCGACCAAGCACTAG	SEQ ID NO: 1601
		Reverse Primer	CTTCAACCACCTTCCCAAAC	SEQ ID NO: 1602
PDGFRb	NM_002609.2	Forward Primer	CCAGCTCTCCTTCCAGCTAC	SEQ ID NO: 1603
		Probe	ATCAATGTCCCTGTCCGAGTGCTG	SEQ ID NO: 1604
		Reverse Primer	GGGTGGCTCTCACTTAGCTC	SEQ ID NO: 1605
PFN1	NM_005022.2	Forward Primer	GGAAAACGTTCGTCAACATC	SEQ ID NO: 1606
		Probe	CAACCAGGACACCCACCTCAGCT	SEQ ID NO: 1607
		Reverse Primer	AAAACTTGACCGGTCTTTGC	SEQ ID NO: 1608
PFN2	NM_053024.1	Forward Primer	TCTATACGTCGATGGTGACTGC	SEQ ID NO: 1609
		Probe	CTCCCCACCTTGACTCTTTGTCCG	SEQ ID NO: 1610
		Reverse Primer	GCCGACAGCCACATTGTAT	SEQ ID NO: 1611
PGK1	NM_000291.1	Forward Primer	AGAGCCAGTTGCTGTAGAACTCAA	SEQ ID NO: 1612
		Probe	TCTCTGCTGGGCAAGGATGTTCTGTTC	SEQ ID NO: 1613
		Reverse Primer	CTGGGCCTACACAGTCCTTCA	SEQ ID NO: 1614
PI3K	NM_002646.2	Forward Primer	TGCTACCTGGACAGCCCG	SEQ ID NO: 1615
		Probe	TCCTCCTGAAACGAGCTGTGTCTGACTT	SEQ ID NO: 1616
		Reverse Primer	AGGCCGTCCTTCAGTAACCA	SEQ ID NO: 1617
PI3KC2A	NM_002645.1	Forward Primer	ATACCAATCACCGCACAAACC	SEQ ID NO: 1618
		Probe	TGCGCTGTGACTGGACTTAACAAATAGCCT	SEQ ID NO: 1619
		Reverse Primer	CACACTAGCATTTTCTCCGCATA	SEQ ID NO: 1620
PIK3CA	NM_006218.1	Forward Primer	GTGATTGAAGAGCATGCCAA	SEQ ID NO: 1621
		Probe	TCCTGCTTCTCGGGATACAGACCA	SEQ ID NO: 1622
		Reverse Primer	GTCCTGCGTGGGAATAGC	SEQ ID NO: 1623
PIM1	NM_002648.2	Forward Primer	CTGCTCAAGGACACCGTCTA	SEQ ID NO: 1624
		Probe	TACACTCGGGTCCCATCGAAGTCC	SEQ ID NO: 1625
		Reverse Primer	GGATCCACTCTGGAGGGC	SEQ ID NO: 1626
Pin1	NM_006221.1	Forward Primer	GATCAACGGCTACATCCAGA	SEQ ID NO: 1627
		Probe	TCAAAGTCCTCCTCTCCCGACTTGA	SEQ ID NO: 1628
		Reverse Primer	TGAACTGTGAGGCCAGAGAC	SEQ ID NO: 1629
PKD1	NM_000296.2	Forward Primer	CAGCACCAGCGATTACGAC	SEQ ID NO: 1630
		Probe	AGCCATTGTGAGGACTCTCCCAGC	SEQ ID NO: 1631
		Reverse Primer	CTGAATAGGCCCACGTCC	SEQ ID NO: 1632
PKR2	NM_002654.3	Forward Primer	CCGCCTGGACATTGATTCAC	SEQ ID NO: 1633
		Probe	ACCCATCACAGCCCGGAACACTG	SEQ ID NO: 1634
		Reverse Primer	CTGGGCCAATGGTACAGATGA	SEQ ID NO: 1635
PLA2G2A	NM_000300.2	Forward Primer	GCATCCCTCACCCATCCTA	SEQ ID NO: 1636
		Probe	AGGCCAGGCAGGAGCCCTTCTATA	SEQ ID NO: 1637
		Reverse Primer	GCTGGAAATCTGCTGGATGT	SEQ ID NO: 1638
PLAUR	NM_002659.1	Forward Primer	CCCATGGATGCTCCTCTGAA	SEQ ID NO: 1639
		Probe	CATTGACTGCCGAGGCCCCATG	SEQ ID NO: 1640
		Reverse Primer	CCGGTGGCTACCAGACATTG	SEQ ID NO: 1641
PLK	NM_005030.2	Forward Primer	AATGAATACAGTATTCCCAAGCACAT	SEQ ID NO: 1642
		Probe	AACCCCGTGGCCGCCTCC	SEQ ID NO: 1643
		Reverse Primer	TGTCTGAAGCATCTTCTGGATGA	SEQ ID NO: 1644
PLK3	NM_004073.2	Forward Primer	TGAAGGAGACGTACCGCTG	SEQ ID NO: 1645
		Probe	CAAGCAGGTTCACTACACGCTGCC	SEQ ID NO: 1646
		Reverse Primer	CAGGCAGTGAGAGGCTGG	SEQ ID NO: 1647
PLOD2	NM_000935.2	Forward Primer	CAGGGAGGTGGTTGCAAAT	SEQ ID NO: 1648
		Probe	TCCAGCCTTTTCGTGGTGACTCAA	SEQ ID NO: 1649
		Reverse Primer	TCTCCCAGGATGCATGAAG	SEQ ID NO: 1650

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
PMS1	NM_000534.2	Forward Primer	CTTACGGTTTTCGTGGAGAAG	SEQ ID NO: 1651
		Probe	CCTCAGCTATACAACAAATTGACCCCAAG	SEQ ID NO: 1652
		Reverse Primer	AGCAGCCGTTCTTGTTGTAA	SEQ ID NO: 1653
PMS2	NM_000535.2	Forward Primer	GATGTGGACTGCCATTCAAA	SEQ ID NO: 1654
		Probe	TCGAAATTTACATCCGGTATCTTCCTGG	SEQ ID NO: 1655
		Reverse Primer	TGCGAGATTAGTTGGCTGAG	SEQ ID NO: 1656
PPARG	NM_005037.3	Forward Primer	TGACTTTATGGAGCCCAAGTT	SEQ ID NO: 1657
		Probe	TTCCAGTGCATTGAACTTCACAGCA	SEQ ID NO: 1658
		Reverse Primer	GCCAAGTCGCTGTCATCTAA	SEQ ID NO: 1659
PPID	NM_005038.1	Forward Primer	TCCTCATTTGGATGGGAAAC	SEQ ID NO: 1660
		Probe	TTCCTTTAATTACTTGGCCAAACACCACA	SEQ ID NO: 1661
		Reverse Primer	CCAATATCCTTGCCACTCCTA	SEQ ID NO: 1662
PPM1D	NM_003620.1	Forward Primer	GCCATCCGCAAAGGCTTT	SEQ ID NO: 1663
		Probe	TCGCTTGTCACCTTGCCATGTGG	SEQ ID NO: 1664
		Reverse Primer	GGCCATTCCGCCAGTTTC	SEQ ID NO: 1665
PPP2R4	NM_178001.1	Forward Primer	GGCTCAGAGCATAAGGCTTC	SEQ ID NO: 1666
		Probe	TTGGTCACTTCTCCCAACTTGGGC	SEQ ID NO: 1667
		Reverse Primer	ACGGGAACTCAGAAAACTGG	SEQ ID NO: 1668
PR	NM_000926.2	Forward Primer	GCATCAGGCTGTCATTATGG	SEQ ID NO: 1669
		Probe	TGTCCTTACCTGTGGGAGCTGTAAGGTC	SEQ ID NO: 1670
		Reverse Primer	AGTAGTTGTGCTGCCCTTCC	SEQ ID NO: 1671
PRDX2	NM_005809.4	Forward Primer	GGTGTCCTTCGCCAGATCAC	SEQ ID NO: 1672
		Probe	TTAATGATTTGCCTGTGGGACGCTCC	SEQ ID NO: 1673
		Reverse Primer	CAGCCGCAGAGCCTCATC	SEQ ID NO: 1674
PRDX3	NM_006793.2	Forward Primer	TGACCCCAATGGAGTCATCA	SEQ ID NO: 1675
		Probe	CATTTGAGCGTCAACGATCTCCCAGTG	SEQ ID NO: 1676
		Reverse Primer	CCAAGCGGAGGGTTTCTTC	SEQ ID NO: 1677
PRDX4	NM_006406.1	Forward Primer	TTACCCATTTGGCCTGGATTAA	SEQ ID NO: 1678
		Probe	CCAAGTCCTCCTTGTCTTCGAGGGGT	SEQ ID NO: 1679
		Reverse Primer	CTGAAAGAAGTGGAATCCTTATTGG	SEQ ID NO: 1680
PRDX6	NM_004905.2	Forward Primer	CTGTGAGCCAGAGGATGTCA	SEQ ID NO: 1681
		Probe	CTGCCAATTGTGTTTTCCTGCAGC	SEQ ID NO: 1682
		Reverse Primer	TGTGATGACACCAGGATGTG	SEQ ID NO: 1683
PRKCA	NM_002737.1	Forward Primer	CAAGCAATGCGTCATCAATGT	SEQ ID NO: 1684
		Probe	CAGCCTCTGCGGAATGGATCACACT	SEQ ID NO: 1685
		Reverse Primer	GTAAATCCGCCCCCTCTTCT	SEQ ID NO: 1686
PRKCB1	NM_002738.5	Forward Primer	GACCCAGCTCCACTCCTG	SEQ ID NO: 1687
		Probe	CCAGACCATGGACCGCCTGTACTT	SEQ ID NO: 1688
		Reverse Primer	CCCATTCACGTACTCCATCA	SEQ ID NO: 1689
PRKCD	NM_006254.1	Forward Primer	CTGACACTTGCCGCAGAGAA	SEQ ID NO: 1690
		Probe	CCCTTTCTCACCCACCTCATCTGCAC	SEQ ID NO: 1691
		Reverse Primer	AGGTGGTCCTTGGTCTGGAA	SEQ ID NO: 1692
PRKR	NM_002759.1	Forward Primer	GCGATACATGAGCCCAGAACA	SEQ ID NO: 1693
		Probe	AGGTCCACTTCCTTTCCATAGTCTTGCGA	SEQ ID NO: 1694
		Reverse Primer	TCAGCAAGAATTAGCCCCAAAG	SEQ ID NO: 1695
pS2	NM_003225.1	Forward Primer	GCCCTCCCAGTGTGCAAAT	SEQ ID NO: 1696
		Probe	TGCTGTTTCGACGACACCGTTCG	SEQ ID NO: 1697
		Reverse Primer	CGTCGATGGTATTAGGATAGAAGCA	SEQ ID NO: 1698
PTCH	NM_000264.2	Forward Primer	CCACGACAAAGCCGACTAC	SEQ ID NO: 1699
		Probe	CCTGAAACAAGGCTGAGAATCCCG	SEQ ID NO: 1700
		Reverse Primer	TACTCGATGGGCTCTGCTG	SEQ ID NO: 1701
PTEN	NM_000314.1	Forward Primer	TGGCTAAGTGAAGATGACAATCATG	SEQ ID NO: 1702
		Probe	CCTTTCCAGCTTTACAGTGAATTGCTGCA	SEQ ID NO: 1703
		Reverse Primer	TGCACATATCATTACACCAGTTCGT	SEQ ID NO: 1704
PTGER3	NM_000957.2	Forward Primer	TAACTGGGGCAACCTTTTCT	SEQ ID NO: 1705
		Probe	CCTTTGCCTTCCTGGGGCTCTT	SEQ ID NO: 1706
		Reverse Primer	TTGCAGGAAAAGGTGACTGT	SEQ ID NO: 1707

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
PTHLH	NM_002820.1	Forward Primer	AGTGACTGGGAGTGGGCTAGAA	SEQ ID NO: 1708
		Probe	TGACACCTCCACAACGTCGCTGGA	SEQ ID NO: 1709
		Reverse Primer	AAGCCTGTTACCGTGAATCGA	SEQ ID NO: 1710
PTHR1	NM_000316.1	Forward Primer	CGAGGTACAAGCTGAGATCAAGAA	SEQ ID NO: 1711
		Probe	CCAGTGCCAGTGTCCAGCGGCT	SEQ ID NO: 1712
		Reverse Primer	GCGTGCCTTTCGCTTGAA	SEQ ID NO: 1713
PTK2	NM_005607.3	Forward Primer	GACCGGTCGAATGATAAGGT	SEQ ID NO: 1714
		Probe	ACCAGGCCCGTCACATTCTCGTAC	SEQ ID NO: 1715
		Reverse Primer	CTGGACATCTCGATGACAGC	SEQ ID NO: 1716
PTK2B	NM_004103.3	Forward Primer	CAAGCCCAGCCGACCTAAG	SEQ ID NO: 1717
		Probe	CTCCGCAAACCAACCTCCTGGCT	SEQ ID NO: 1718
		Reverse Primer	GAACCTGGAACTGCAGCTTTG	SEQ ID NO: 1719
PTP4A3	NM_007079.2	Forward Primer	CCTGTTCTCGGCACCTTAAA	SEQ ID NO: 1720
		Probe	ACCTGACTGCCCCGGGGTCTAATA	SEQ ID NO: 1721
		Reverse Primer	TATTGCCTTCGGGTGTCC	SEQ ID NO: 1722
PTP4A3 v2	NM_032611.1	Forward Primer	AATATTTGTGCGGGGTATGG	SEQ ID NO: 1723
		Probe	CCAAGAGAAACGAGATTTAAAAACCCACC	SEQ ID NO: 1724
		Reverse Primer	AACGAGATCCCTGTGCTTGT	SEQ ID NO: 1725
PTPD1	NM_007039.2	Forward Primer	CGCTTGCCTAACTCATACTTTCC	SEQ ID NO: 1726
		Probe	TCCACGCAGCGTGGCACTG	SEQ ID NO: 1727
		Reverse Primer	CCATTCAGACTGCGCCACTT	SEQ ID NO: 1728
PTPN1	NM_002827.2	Forward Primer	AATGAGGAAGTTTCGGATGG	SEQ ID NO: 1729
		Probe	CTGATCCAGACAGCCGACCAGCT	SEQ ID NO: 1730
		Reverse Primer	CTTCGATCACAGCCAGGTAG	SEQ ID NO: 1731
PTPRF	NM_002840.2	Forward Primer	TGTTTTAGCTGAGGGACGTG	SEQ ID NO: 1732
		Probe	CCGACGTCCCCAAACCTAGCTAGG	SEQ ID NO: 1733
		Reverse Primer	TACCAACCCTGGAATGTTGA	SEQ ID NO: 1734
PTPRJ	NM_002843.2	Forward Primer	AACTTCCGGTACCTCGTTCGT	SEQ ID NO: 1735
		Probe	ACTACATGAAGCAGAGTCCTCCCGAATCG	SEQ ID NO: 1736
		Reverse Primer	AGCACTGCAATGCACCAGAA	SEQ ID NO: 1737
PTPRO	NM_030667.1	Forward Primer	CATGGCCTGATCATGGTGT	SEQ ID NO: 1738
		Probe	CCCACAGCAAATGCTGCAGAAAGT	SEQ ID NO: 1739
		Reverse Primer	CCATGTGTACAAACTGCAGGA	SEQ ID NO: 1740
PTTG1	NM_004219.2	Forward Primer	GGCTACTCTGATCTATGTTGATAAGGAA	SEQ ID NO: 1741
		Probe	CACACGGGTGCCTGGTTCTCCA	SEQ ID NO: 1742
		Reverse Primer	GCTTCAGCCCATCCTTAGCA	SEQ ID NO: 1743
RAB32	NM_006834.2	Forward Primer	CCTGCAGCTGTGGGACAT	SEQ ID NO: 1744
		Probe	CGATTTGGCAACATGACCCGAGTA	SEQ ID NO: 1745
		Reverse Primer	AGCACCAACAGCTTCCTTG	SEQ ID NO: 1746
RAB6C	NM_032144.1	Forward Primer	GCGACAGCTCCTCTAGTTCCA	SEQ ID NO: 1747
		Probe	TTCCCGAAGTCTCCGCCCG	SEQ ID NO: 1748
		Reverse Primer	GGAACACCAGCTTGAATTTCCT	SEQ ID NO: 1749
RAC1	NM_006908.3	Forward Primer	TGTTGTAAATGTCTCAGCCCC	SEQ ID NO: 1750
		Probe	CGTTCTTGGTCCTGTCCCTTGGA	SEQ ID NO: 1751
		Reverse Primer	TTGAGCAAAGCGTACAAAGG	SEQ ID NO: 1752
RAD51C	NM_058216.1	Forward Primer	GAACTTCTTGAGCAGGAGCATACC	SEQ ID NO: 1753
		Probe	AGGGCTTCATAATCACCTTCTGTTC	SEQ ID NO: 1754
		Reverse Primer	TCCACCCCCAAGAATATCATCTAGT	SEQ ID NO: 1755
RAD54L	NM_003579.2	Forward Primer	AGCTAGCCTCAGTGACACACATG	SEQ ID NO: 1756
		Probe	ACACAACGTCGGCAGTGCAACCTG	SEQ ID NO: 1757
		Reverse Primer	CCGGATCTGACGGCTGTT	SEQ ID NO: 1758
RAF1	NM_002880.1	Forward Primer	CGTCGTATGCGAGAGTCTGT	SEQ ID NO: 1759
		Probe	TCCAGGATGCCTGTTAGTTCTCAGCA	SEQ ID NO: 1760
		Reverse Primer	TGAAGGCGTGAGGTGTAGAA	SEQ ID NO: 1761
RALBP1	NM_006788.2	Forward Primer	GGTGTCAGATATAAATGTGCAAATGC	SEQ ID NO: 1762
		Probe	TGCTGTCCTGTCGGTCTCAGTACGTTCA	SEQ ID NO: 1763
		Reverse Primer	TTCGATATTGCCAGCAGCTATAAA	SEQ ID NO: 1764

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
RANBP2	NM_006267.3	Forward Primer	TCCTTCAGCTTTCACACTGG	SEQ ID NO: 1765
		Probe	TCCAGAAGAGTCATGCAACTTCATTTCTG	SEQ ID NO: 1766
		Reverse Primer	AAATCCTGTTCCCACCTGAC	SEQ ID NO: 1767
ranBP7	NM_006391.1	Forward Primer	AACATGATTATCCAAGCCGC	SEQ ID NO: 1768
		Probe	AAGCCAATTTTGTCCACAATGGCA	SEQ ID NO: 1769
		Reverse Primer	GCCAACAAGCACTGTTATCG	SEQ ID NO: 1770
RANBP9	NM_005493.2	Forward Primer	CAAGTCAGTTGAGACGCCAGTT	SEQ ID NO: 1771
		Probe	TTCTATGGCGGCCTGACTTCCTCCA	SEQ ID NO: 1772
		Reverse Primer	TGCAGCTCTCGTCCAAAGTG	SEQ ID NO: 1773
RAP1GDS1	NM_021159.3	Forward Primer	TGTGGATGCTGGATTGATTT	SEQ ID NO: 1774
		Probe	CCACTGGTGCAGCTGCTAAATAGCA	SEQ ID NO: 1775
		Reverse Primer	AAGCAGCACTTCCTGGTCTT	SEQ ID NO: 1776
RARA	NM_000964.1	Forward Primer	AGTCTGTGAGAAACGACCGAAAC	SEQ ID NO: 1777
		Probe	TCGGGCTTGGGCACCTCCTTCTT	SEQ ID NO: 1778
		Reverse Primer	CGGCGTCAGCGTGTAGCT	SEQ ID NO: 1779
RARB	NM_016152.2	Forward Primer	TGCCTGGACATCCTGATTCT	SEQ ID NO: 1780
		Probe	TGCACCAGGTATACCCCAGAACAAGA	SEQ ID NO: 1781
		Reverse Primer	AAGGCCGTCTGAGAAAGTCA	SEQ ID NO: 1782
RASSF1	NM_007182.3	Forward Primer	AGTGGGAGACACCTGACCTT	SEQ ID NO: 1783
		Probe	TTGATCTTCTGCTCAATCTCAGCTTGAGA	SEQ ID NO: 1784
		Reverse Primer	TGATCTGGGCATTGTACTCC	SEQ ID NO: 1785
RBM5	NM_005778.1	Forward Primer	CGAGAGGGAGAGCAAGACCAT	SEQ ID NO: 1786
		Probe	CTGCGCGGCCTTCCCATCA	SEQ ID NO: 1787
		Reverse Primer	TCTCGAATATCGCTCTCTGTGATG	SEQ ID NO: 1788
RBX1	NM_014248.2	Forward Primer	GGAACCACATTATGGATCTTTGC	SEQ ID NO: 1789
		Probe	TAGAATGTCAAGCTAACCAGGCGTCCGC	SEQ ID NO: 1790
		Reverse Primer	CATGCGACAGTACACTCTTCTGAA	SEQ ID NO: 1791
RCC1	NM_001269.2	Forward Primer	GGGCTGGGTGAGAATGTG	SEQ ID NO: 1792
		Probe	ATACCAGGGCCGGCTTCTTCCTCT	SEQ ID NO: 1793
		Reverse Primer	CACAACATCCTCCGGAATG	SEQ ID NO: 1794
REG4	NM_032044.2	Forward Primer	TGCTAACTCCTGCACAGCC	SEQ ID NO: 1795
		Probe	TCCTCTTCCTTTCTGCTAGCCTGGC	SEQ ID NO: 1796
		Reverse Primer	TGCTAGGTTTCCCCTCTGAA	SEQ ID NO: 1797
RFC	NM_003056.1	Forward Primer	TCAAGACCATCATCACTTTCATTGT	SEQ ID NO: 1798
		Probe	CCTCCCGGTCCGCAAGCAGTT	SEQ ID NO: 1799
		Reverse Primer	GGATCAGGAAGTACACGGAGTATAACT	SEQ ID NO: 1800
RhoB	NM_004040.2	Forward Primer	AAGCATGAACAGGACTTGACC	SEQ ID NO: 1801
		Probe	CTTTCCAACCCCTGGGGAAGACAT	SEQ ID NO: 1802
		Reverse Primer	CCTCCCCAAGTCAGTTGC	SEQ ID NO: 1803
rhoC	NM_175744.1	Forward Primer	CCCGTTCGGTCTGAGGAA	SEQ ID NO: 1804
		Probe	TCCGGTTCGCCATGTCCCG	SEQ ID NO: 1805
		Reverse Primer	GAGCACTCAAGGTAGCCAAAGG	SEQ ID NO: 1806
RIZ1	NM_012231.1	Forward Primer	CCAGACGAGCGATTAGAAGC	SEQ ID NO: 1807
		Probe	TGTGAGGTGAATGATTTGGGGGA	SEQ ID NO: 1808
		Reverse Primer	TCCTCCTCTTCCTCCTCCTC	SEQ ID NO: 1809
RNF11	NM_014372.3	Forward Primer	ACCCTGGAAGAGATGGATCA	SEQ ID NO: 1810
		Probe	CCATCATACAGATCACACACTCCCGG	SEQ ID NO: 1811
		Reverse Primer	ATTGGGTCCCCATAAACAAA	SEQ ID NO: 1812
ROCK1	NM_005406.1	Forward Primer	TGTGCACATAGGAATGAGCTTC	SEQ ID NO: 1813
		Probe	TCACTCTCTTTGCTGGCCAACTGC	SEQ ID NO: 1814
		Reverse Primer	GTTTAGCACGCAATTGCTCA	SEQ ID NO: 1815
ROCK2	NM_004850.3	Forward Primer	GATCCGAGACCCTCGCTC	SEQ ID NO: 1816
		Probe	CCCATCAACGTGGAGAGCTTGCT	SEQ ID NO: 1817
		Reverse Primer	AGGACCAAGGAATTTAAGCCA	SEQ ID NO: 1818
RPLPO	NM_001002.2	Forward Primer	CCATTCTATCATCAACGGGTACAA	SEQ ID NO: 1819
		Probe	TCTCCACAGACAAGGCCAGGACTCG	SEQ ID NO: 1820
		Reverse Primer	TCAGCAAGTGGGAAGGTGTAATC	SEQ ID NO: 1821

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
RPS13	NM_001017.2	Forward Primer	CAGTCGGCTTTACCCTATCG	SEQ ID NO: 1822
		Probe	CAACTTCAACCAAGTGGGGACGCT	SEQ ID NO: 1823
		Reverse Primer	TCTGCTCCTTCACGTCGTC	SEQ ID NO: 1824
RRM1	NM_001033.1	Forward Primer	GGGCTACTGGCAGCTACATT	SEQ ID NO: 1825
		Probe	CATTGGAATTGCCATTAGTCCCAGC	SEQ ID NO: 1826
		Reverse Primer	CTCTCAGCATCGGTACAAGG	SEQ ID NO: 1827
RRM2	NM_001034.1	Forward Primer	CAGCGGGATTAAACAGTCCT	SEQ ID NO: 1828
		Probe	CCAGCACAGCCAGTTAAAAGATGCA	SEQ ID NO: 1829
		Reverse Primer	ATCTGCGTTGAAGCAGTGAG	SEQ ID NO: 1830
RTN4	NM_007008.1	Forward Primer	GACTGGAGTGGTGTTTGGTG	SEQ ID NO: 1831
		Probe	CCAGCCTATTCCTGCTGCTTTCATTG	SEQ ID NO: 1832
		Reverse Primer	CTGTTACGCTCACAATGCTG	SEQ ID NO: 1833
RUNX1	NM_001754.2	Forward Primer	AACAGAGACATTGCCAACCA	SEQ ID NO: 1834
		Probe	TTGGATCTGCTTGCTGTCCAAACC	SEQ ID NO: 1835
		Reverse Primer	GTGATTTGCCCAGGAAGTTT	SEQ ID NO: 1836
RXRA	NM_002957.3	Forward Primer	GCTCTGTTGTGTCCTGTTGC	SEQ ID NO: 1837
		Probe	TCAGTCACAGGAAGGCCAGAGCC	SEQ ID NO: 1838
		Reverse Primer	GTACGGAGAAGCCACTTCACA	SEQ ID NO: 1839
S100A1	NM_006271.1	Forward Primer	TGGACAAGGTGATGAAGGAG	SEQ ID NO: 1840
		Probe	CCTCCCCGTCTCCATTCTCGTCTA	SEQ ID NO: 1841
		Reverse Primer	AGCACCACATACTCCTGGAA	SEQ ID NO: 1842
S100A2	NM_005978.2	Forward Primer	TGGCTGTGCTGGTCACTACCT	SEQ ID NO: 1843
		Probe	CACAAGTACTCCTGCCAAGAGGGCGAC	SEQ ID NO: 1844
		Reverse Primer	TCCCCCTTACTCAGCTTGAACT	SEQ ID NO: 1845
S100A4	NM_002961.2	Forward Primer	GACTGCTGTCATGGCGTG	SEQ ID NO: 1846
		Probe	ATCACATCCAGGGCCTTCTCCAGA	SEQ ID NO: 1847
		Reverse Primer	CGAGTACTTGTGGAAGGTGGAC	SEQ ID NO: 1848
S100A8	NM_002964.3	Forward Primer	ACTCCCTGATAAAGGGGAATTT	SEQ ID NO: 1849
		Probe	CATGCCGTCTACAGGGATGACCTG	SEQ ID NO: 1850
		Reverse Primer	TGAGGACACTCGGTCTCTAGC	SEQ ID NO: 1851
S100A9	NM_002965.2	Forward Primer	CTTTGGGACAGAGTGCAAGA	SEQ ID NO: 1852
		Probe	CGATGACTTGCAAAATGTCGCAGC	SEQ ID NO: 1853
		Reverse Primer	TGGTCTCTATGTTGCGTTCC	SEQ ID NO: 1854
S100P	NM_005980.2	Forward Primer	AGACAAGGATGCCGTGGATAA	SEQ ID NO: 1855
		Probe	TTGCTCAAGGACCTGGACGCCAA	SEQ ID NO: 1856
		Reverse Primer	GAAGTCCACCTGGGCATCTC	SEQ ID NO: 1857
SAT	NM_002970.1	Forward Primer	CCTTTTACCACTGCCTGGTT	SEQ ID NO: 1858
		Probe	TCCAGTGCTCTTTCGGCACTTCTG	SEQ ID NO: 1859
		Reverse Primer	ACAATGCTGTGTCCTTCCG	SEQ ID NO: 1860
SBA2	NM_018639.3	Forward Primer	GGACTCAACGATGGGCAG	SEQ ID NO: 1861
		Probe	CCCTGTCTGCACCTCCCAGATCTT	SEQ ID NO: 1862
		Reverse Primer	CGGAAAGATTCAAAAGCAGG	SEQ ID NO: 1863
SDC1	NM_002997.1	Forward Primer	GAAATTGACGAGGGGTGTCT	SEQ ID NO: 1864
		Probe	CTCTGAGCGCCTCCATCCAAGG	SEQ ID NO: 1865
		Reverse Primer	AGGAGCTAACGGAGAACCTG	SEQ ID NO: 1866
SEMA3B	NM_004636.1	Forward Primer	GCTCCAGGATGTGTTTCTGTTG	SEQ ID NO: 1867
		Probe	TCGCGGGACCACCGGACC	SEQ ID NO: 1868
		Reverse Primer	ACGTGGAGAAGACGGCATAGA	SEQ ID NO: 1869
SEMA3F	NM_004186.1	Forward Primer	CGCGAGCCCCTCATTATACA	SEQ ID NO: 1870
		Probe	CTCCCCACAGCGCATCGAGGAA	SEQ ID NO: 1871
		Reverse Primer	CACTCGCCGTTGACATCCT	SEQ ID NO: 1872
SEMA4B	NM_020210.1	Forward Primer	TTCCAGCCCAACACAGTGAA	SEQ ID NO: 1873
		Probe	ACTTTGGCCTGCCCGCTCCTCT	SEQ ID NO: 1874
		Reverse Primer	GAGTCGGGTCGCCAGGTT	SEQ ID NO: 1875
SFRP2	NM_003013.2	Forward Primer	CAAGCTGAACGGTGTGTCC	SEQ ID NO: 1876
		Probe	CAGCACCGATTTCTTCAGGTCCCT	SEQ ID NO: 1877
		Reverse Primer	TGCAAGCTGTCTTTGAGCC	SEQ ID NO: 1878

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
SFRP4	NM_003014.2	Forward Primer	TACAGGATGAGGCTGGGC	SEQ ID NO: 1879
		Probe	CCTGGGACAGCCTATGTAAGGCCA	SEQ ID NO: 1880
		Reverse Primer	GTTGTTAGGGCAAGGGGC	SEQ ID NO: 1881
SGCB	NM_000232.1	Forward Primer	CAGTGGAGACCAGTTGGGTAGTG	SEQ ID NO: 1882
		Probe	CACACATGCAGAGCTTGTAGCGTACCCA	SEQ ID NO: 1883
		Reverse Primer	CCTTGAAGAGCGTCCCATCA	SEQ ID NO: 1884
SHC1	NM_003029.3	Forward Primer	CCAACACCTTCTTGGCTTCT	SEQ ID NO: 1885
		Probe	CCTGTGTTCTTGCTGAGCACCCTC	SEQ ID NO: 1886
		Reverse Primer	CTGTTATCCCAACCCAAACC	SEQ ID NO: 1887
SHH	NM_000193.2	Forward Primer	GTCCAAGGCACATATCCACTG	SEQ ID NO: 1888
		Probe	CACCGAGTTCTCTGCTTTCACCGA	SEQ ID NO: 1889
		Reverse Primer	GAAGCAGCCTCCCGATTT	SEQ ID NO: 1890
SI	NM_001041.1	Forward Primer	AACGGACTCCCTCAATTTGT	SEQ ID NO: 1891
		Probe	TGTCCATGGTCATGCAAATCTTGC	SEQ ID NO: 1892
		Reverse Primer	GAAATTGCAGGGTCCAAGAT	SEQ ID NO: 1893
Siah-1	NM_003031.2	Forward Primer	TTGGCATTGGAACTACATTCA	SEQ ID NO: 1894
		Probe	TCCGCGGTATCCTCGGATTAGTTC	SEQ ID NO: 1895
		Reverse Primer	GGTATGGAGAAGGGGGTCC	SEQ ID NO: 1896
SIAT4A	NM_003033.2	Forward Primer	AACCACAGTTGGAGGAGGAC	SEQ ID NO: 1897
		Probe	CAGAGACAGTTTCCCTCCCCGCT	SEQ ID NO: 1898
		Reverse Primer	CGAAGGAAGGGTGTTGGTAT	SEQ ID NO: 1899
SIAT7B	NM_006456.1	Forward Primer	TCCAGCCCAAATCCTCCT	SEQ ID NO: 1900
		Probe	TGGCACATCCTACCCCAGATGCTA	SEQ ID NO: 1901
		Reverse Primer	GGTGTCCTGGAGTCCTTGAA	SEQ ID NO: 1902
SIM2	NM_005069.2	Forward Primer	GATGGTAGGAAGGGATGTGC	SEQ ID NO: 1903
		Probe	CGCCTCTCCACGCACTCAGCTAT	SEQ ID NO: 1904
		Reverse Primer	CACAAGGAGCTGTGAATGAGG	SEQ ID NO: 1905
SIN3A	NM_015477.1	Forward Primer	CCAGAGTCATGCTCATCCAG	SEQ ID NO: 1906
		Probe	CTGTCCCTGCACTGGTGCAACTG	SEQ ID NO: 1907
		Reverse Primer	CCACCTTCAGCCTCTGAAAT	SEQ ID NO: 1908
SIR2	NM_012238.3	Forward Primer	AGCTGGGGTGTCTGTTTCAT	SEQ ID NO: 1909
		Probe	CCTGACTTCAGGTCAAGGGATGG	SEQ ID NO: 1910
		Reverse Primer	ACAGCAAGGCGAGCATAAAT	SEQ ID NO: 1911
SKP1A	NM_006930.2	Forward Primer	CCATTGCCTTTGCTTTGTTCAT	SEQ ID NO: 1912
		Probe	TCCCATGGTTTTTATTCTGCCCTGCTG	SEQ ID NO: 1913
		Reverse Primer	TTCCGGATTTCCTTTCTTTGC	SEQ ID NO: 1914
SKP2	NM_005983.2	Forward Primer	AGTTGCAGAATCTAAGCCTGGAA	SEQ ID NO: 1915
		Probe	CCTGCGGCTTTCGGATCCCA	SEQ ID NO: 1916
		Reverse Primer	TGAGTTTTTTGCGAGAGTATTGACA	SEQ ID NO: 1917
SLC25A3	NM_213611.1	Forward Primer	TCTGCCAGTGCTGAATTCTT	SEQ ID NO: 1918
		Probe	TGCTGACATTGCCCTGGCTCCTAT	SEQ ID NO: 1919
		Reverse Primer	TTCGAACCTTAGCAGCTTCC	SEQ ID NO: 1920
SLC2A1	NM_006516.1	Forward Primer	GCCTGAGTCTCCTGTGCC	SEQ ID NO: 1921
		Probe	ACATCCCAGGCTTCACCCTGAATG	SEQ ID NO: 1922
		Reverse Primer	AGTCTCCACCCTCAGGCAT	SEQ ID NO: 1923
SLC31A1	NM_001859.2	Forward Primer	CCGTTCGAAGAGTCGTGAG	SEQ ID NO: 1924
		Probe	TCTCCGAATCTTAACCCGTCACCC	SEQ ID NO: 1925
		Reverse Primer	AGTCCAGCCACTAGCACCTC	SEQ ID NO: 1926
SLC5A8	NM_145913.2	Forward Primer	CCTGCTTTCAACCACATTGA	SEQ ID NO: 1927
		Probe	TCCCATTGCTCTTGCCACTCTGAT	SEQ ID NO: 1928
		Reverse Primer	AGAGCAGCTTCACAAACGAG	SEQ ID NO: 1929
SLC7A5	NM_003486.4	Forward Primer	GCGCAGAGGCCAGTTAAA	SEQ ID NO: 1930
		Probe	AGATCACCTCCTCGAACCCACTCC	SEQ ID NO: 1931
		Reverse Primer	AGCTGAGCTGTGGGTTGC	SEQ ID NO: 1932
SLPI	NM_003064.2	Forward Primer	ATGGCCAATGTTTGATGCT	SEQ ID NO: 1933
		Probe	TGGCCATCCATCTCACAGAAATTGG	SEQ ID NO: 1934
		Reverse Primer	ACACTTCAAGTCACGCTTGC	SEQ ID NO: 1935

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
SMARCA3	NM_003071.2	Forward Primer	AGGGACTGTCCTGGCACAT	SEQ ID NO: 1936
		Probe	AGCAAAAGACCCAGGACATCTGCA	SEQ ID NO: 1937
		Reverse Primer	CAACAAATTTGCCGCAGTC	SEQ ID NO: 1938
SNAI1	NM_005985.2	Forward Primer	CCCAATCGGAAGCCTAACTA	SEQ ID NO: 1939
		Probe	TCTGGATTAGAGTCCTGCAGCTCGC	SEQ ID NO: 1940
		Reverse Primer	GTAGGGCTGCTGGAAGGTAA	SEQ ID NO: 1941
SNAI2	NM_003068.3	Forward Primer	GGCTGGCCAAACATAAGCA	SEQ ID NO: 1942
		Probe	CTGCACTGCGATGCCCAGTCTAGAAAATC	SEQ ID NO: 1943
		Reverse Primer	TCCTTGTCACAGTATTTACAGCTGAA	SEQ ID NO: 1944
SNRPF	NM_003095.1	Forward Primer	GGCTGGTCGGCAGAGAGTAG	SEQ ID NO: 1945
		Probe	AAACTCATGTAAACCACGGCCGAATGTTG	SEQ ID NO: 1946
		Reverse Primer	TGAGGAAAGGTTTGGGATTGA	SEQ ID NO: 1947
SOD1	NM_000454.3	Forward Primer	TGAAGAGAGGCATGTTGGAG	SEQ ID NO: 1948
		Probe	TTTGTCAGCAGTCACATTGCCCAA	SEQ ID NO: 1949
		Reverse Primer	AATAGACACATCGGCCACAC	SEQ ID NO: 1950
SOD2	NM_000636.1	Forward Primer	GCTTGTCCAAATCAGGATCCA	SEQ ID NO: 1951
		Probe	AACAACAGGCCTTATTCCACTGCTGGG	SEQ ID NO: 1952
		Reverse Primer	AGCGTGCTCCCACACATCA	SEQ ID NO: 1953
SOS1	NM_005633.2	Forward Primer	TCTGCACCAAATTCTCCAAG	SEQ ID NO: 1954
		Probe	AACACCGTTAACACCTCCGCCTG	SEQ ID NO: 1955
		Reverse Primer	GTGGTACTGGAAGCACCAGA	SEQ ID NO: 1956
SOX17	NM_022454.2	Forward Primer	TCGTGTGCAAGCCTGAGA	SEQ ID NO: 1957
		Probe	CTCCCCTACCAGGGGCATGACTC	SEQ ID NO: 1958
		Reverse Primer	CTGTCGGGGAGATTCACAC	SEQ ID NO: 1959
SPARC	NM_003118.1	Forward Primer	TCTTCCCTGTACACTGGCAGTTC	SEQ ID NO: 1960
		Probe	TGGACCAGCACCCCATTGACGG	SEQ ID NO: 1961
		Reverse Primer	AGCTCGGTGTGGGAGAGGTA	SEQ ID NO: 1962
SPINT2	NM_021102.1	Forward Primer	AGGAATGCAGCGGATTCCT	SEQ ID NO: 1963
		Probe	CCCAAGTGCTCCCAGAAGGCAGG	SEQ ID NO: 1964
		Reverse Primer	TCGCTGGAGTGGTCTTCAGA	SEQ ID NO: 1965
SPRY1	AK026960.1	Forward Primer	CAGACCAGTCCCTGGTCATAGG	SEQ ID NO: 1966
		Probe	CTGGGTCCGGATTGCCCTTTCAG	SEQ ID NO: 1967
		Reverse Primer	CCTTCAAGTCATCCACAATCAGTT	SEQ ID NO: 1968
SPRY2	NM_005842.1	Forward Primer	TGTGGCAAGTGCAAATGTAA	SEQ ID NO: 1969
		Probe	CAGAGGCCTTGGGTAGGTGCACTC	SEQ ID NO: 1970
		Reverse Primer	GTCGCAGATCCAGTCTGATG	SEQ ID NO: 1971
SR-A1	NM_021228.1	Forward Primer	AGATGGAAGAAGCCAACCTG	SEQ ID NO: 1972
		Probe	CTGGATCAGCTCCTGGGCCTTC	SEQ ID NO: 1973
		Reverse Primer	CTGTGGCTGAGGATCTGGT	SEQ ID NO: 1974
ST14	NM_021978.2	Forward Primer	TGACTGCACATGGAACATTG	SEQ ID NO: 1975
		Probe	AGGTGCCCAACAACCAGCATGT	SEQ ID NO: 1976
		Reverse Primer	AAGAATTTGAAGCGCACCTT	SEQ ID NO: 1977
STAT1	NM_007315.1	Forward Primer	GGGCTCAGCTTTCAGAAGTG	SEQ ID NO: 1978
		Probe	TGGCAGTTTTCTTCTGTCACCAAAA	SEQ ID NO: 1979
		Reverse Primer	ACATGTTCAGCTGGTCCACA	SEQ ID NO: 1980
STAT3	NM_003150.1	Forward Primer	TCACATGCCACTTTGGTGTT	SEQ ID NO: 1981
		Probe	TCCTGGGAGAGATTGACCAGCA	SEQ ID NO: 1982
		Reverse Primer	CTTGCAGGAAGCGGCTATAC	SEQ ID NO: 1983
STAT5A	NM_003152.1	Forward Primer	GAGGCGCTCAACATGAAATTC	SEQ ID NO: 1984
		Probe	CGGTTGCTCTGCACTTCGGCCT	SEQ ID NO: 1985
		Reverse Primer	GCCAGGAACACGAGGTTCTC	SEQ ID NO: 1986
STAT5B	NM_012448.1	Forward Primer	CCAGTGGTGGTGATCGTTCA	SEQ ID NO: 1987
		Probe	CAGCCAGGACAACAATGCGACGG	SEQ ID NO: 1988
		Reverse Primer	GCAAAAGCATTGTCCCAGAGA	SEQ ID NO: 1989
STC1	NM_003155.1	Forward Primer	CTCCGAGGTGAGGAGGACT	SEQ ID NO: 1990
		Probe	CACATCAAACGCACATCCCATGAG	SEQ ID NO: 1991
		Reverse Primer	ACCTCTCCCTGGTTATGCAC	SEQ ID NO: 1992

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
STK11	NM_000455.3	Forward Primer	GGACTCGGAGACGCTGTG	SEQ ID NO: 1993
		Probe	TTCTTGAGGATCTTGACGGCCCTC	SEQ ID NO: 1994
		Reverse Primer	GGGATCCTTCGCAACTTCTT	SEQ ID NO: 1995
STK15	NM_003600.1	Forward Primer	CATCTTCCAGGAGGACCACT	SEQ ID NO: 1996
		Probe	CTCTGTGGCACCCTGGACTACCTG	SEQ ID NO: 1997
		Reverse Primer	TCCGACCTTCAATCATTTCA	SEQ ID NO: 1998
STMN1	NM_005563.2	Forward Primer	AATACCCAACGCACAAATGA	SEQ ID NO: 1999
		Probe	CACGTTCTCTGCCCCGTTTCTTG	SEQ ID NO: 2000
		Reverse Primer	GGAGACAATGCAAACCACAC	SEQ ID NO: 2001
STMY3	NM_005940.2	Forward Primer	CCTGGAGGCTGCAACATACC	SEQ ID NO: 2002
		Probe	ATCCTCCTGAAGCCCTTTTCGCAGC	SEQ ID NO: 2003
		Reverse Primer	TACAATGGCTTTGGAGGATAGCA	SEQ ID NO: 2004
STS	NM_000351.2	Forward Primer	GAAGATCCCTTTCCTCCTACTGTTC	SEQ ID NO: 2005
		Probe	CTTCGTGGCTCTCGGCTTCCCA	SEQ ID NO: 2006
		Reverse Primer	GGATGATGTTCGGCCTTGAT	SEQ ID NO: 2007
SURV	NM_001168.1	Forward Primer	TGTTTTGATTCCCGGGCTTA	SEQ ID NO: 2008
		Probe	TGCCTTCTTCCTCCCTCACTTCTCACCT	SEQ ID NO: 2009
		Reverse Primer	CAAAGCTGTCAGCTCTAGCAAAAG	SEQ ID NO: 2010
TAGLN	NM_003186.2	Forward Primer	GATGGAGCAGGTGGCTCAGT	SEQ ID NO: 2011
		Probe	CCCAGAGTCCTCAGCCGCCTTCAG	SEQ ID NO: 2012
		Reverse Primer	AGTCTGGAACATGTCAGTCTTGATG	SEQ ID NO: 2013
TBP	NM_003194.1	Forward Primer	GCCCGAAACGCCGAATATA	SEQ ID NO: 2014
		Probe	TACCGCAGCAAACCGCTTGGG	SEQ ID NO: 2015
		Reverse Primer	CGTGGCTCTCTTATCCTCATGAT	SEQ ID NO: 2016
TCF-1	NM_000545.3	Forward Primer	GAGGTCCTGAGCACTGCC	SEQ ID NO: 2017
		Probe	CTGGGTTCACAGGCTCCTTTGTCC	SEQ ID NO: 2018
		Reverse Primer	GATGTGGGACCATGCTTGT	SEQ ID NO: 2019
TCF-7	NM_003202.2	Forward Primer	GCAGCTGCAGTCAACAGTTC	SEQ ID NO: 2020
		Probe	AAGTCATGGCCCAAATCCAGTGTG	SEQ ID NO: 2021
		Reverse Primer	CTGTGAATGGGGAGGGGT	SEQ ID NO: 2022
TCF7L1	NM_031283.1	Forward Primer	CCGGGACACTTTCCAGAAG	SEQ ID NO: 2023
		Probe	TCTCACTTCGGCGAAATAGTCCCG	SEQ ID NO: 2024
		Reverse Primer	AGAACGCGCTGTCCTGAG	SEQ ID NO: 2025
TCF7L2	NM_030756.1	Forward Primer	CCAATCACGACAGGAGGATT	SEQ ID NO: 2026
		Probe	AGACACCCCTACCCCACAGCTCTG	SEQ ID NO: 2027
		Reverse Primer	TGGACACGGAAGCATTGAC	SEQ ID NO: 2028
TCFL4	NM_170607.2	Forward Primer	CTGACTGCTCTGCTTAAAGGTGAA	SEQ ID NO: 2029
		Probe	TAGCAGGAACAACAACAAAAGCCAACCAA	SEQ ID NO: 2030
		Reverse Primer	ATGTCTTGCACTGGCTACCTTGT	SEQ ID NO: 2031
TEK	NM_000459.1	Forward Primer	ACTTCGGTGCTACTTAACAACTTACATC	SEQ ID NO: 2032
		Probe	AGCTCGGACCACGTACTGCTCCCTG	SEQ ID NO: 2033
		Reverse Primer	CCTGGGCCTTGGTGTTGAC	SEQ ID NO: 2034
TERC	U86046.1	Forward Primer	AAGAGGAACGGAGCGAGTC	SEQ ID NO: 2035
		Probe	CACGTCCCACAGCTCAGGGAATC	SEQ ID NO: 2036
		Reverse Primer	ATGTGTGAGCCGAGTCCTG	SEQ ID NO: 2037
TERT	NM_003219.1	Forward Primer	GACATGGAGAACAAGCTGTTTGC	SEQ ID NO: 2038
		Probe	ACCAAACGCAGGAGCAGCCCG	SEQ ID NO: 2039
		Reverse Primer	GAGGTGTCACCAACAAGAAATCAT	SEQ ID NO: 2040
TFF3	NM_003226.1	Forward Primer	AGGCACTGTTCATCTCAGTTTTTCT	SEQ ID NO: 2041
		Probe	CAGAAAGCTTGCCGGGAGCAAAGG	SEQ ID NO: 2042
		Reverse Primer	CATCAGGCTCCAGATATGAACTTTC	SEQ ID NO: 2043
TGFA	NM_003236.1	Forward Primer	GGTGTGCCACAGACCTTCCT	SEQ ID NO: 2044
		Probe	TTGGCCTGTAATCACCTGTGCAGCCTT	SEQ ID NO: 2045
		Reverse Primer	ACGGAGTTCTTGACAGAGTTTTGA	SEQ ID NO: 2046
TGFB2	NM_003238.1	Forward Primer	ACCAGTCCCCCAGAAGACTA	SEQ ID NO: 2047
		Probe	TCCTGAGCCCGAGGAAGTCCC	SEQ ID NO: 2048
		Reverse Primer	CCTGGTGCTGTTGTAGATGG	SEQ ID NO: 2049

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
TGFB3	NM_003239.1	Forward Primer	GGATCGAGCTCTTCCAGATCCT	SEQ ID NO: 2050
		Probe	CGGCCAGATGAGCACATTGCC	SEQ ID NO: 2051
		Reverse Primer	GCCACCGATATAGCGCTGTT	SEQ ID NO: 2052
TGFBI	NM_000358.1	Forward Primer	GCTACGAGTGCTGTCCTGG	SEQ ID NO: 2053
		Probe	CCTTCTCCCCAGGGACCTTTTCAT	SEQ ID NO: 2054
		Reverse Primer	AGTGGTAGGGCTGCTGGAC	SEQ ID NO: 2055
TGFBR1	NM_004612.1	Forward Primer	GTCATCACCTGGCCTTGG	SEQ ID NO: 2056
		Probe	AGCAATGACAGCTGCCAGTTCCAC	SEQ ID NO: 2057
		Reverse Primer	GCAGACGAAGCACACTGGT	SEQ ID NO: 2058
TGFBR2	NM_003242.2	Forward Primer	AACACCAATGGGTTCCATCT	SEQ ID NO: 2059
		Probe	TTCTGGGCTCCTGATTGCTCAAGC	SEQ ID NO: 2060
		Reverse Primer	CCTCTTCATCAGGCCAAACT	SEQ ID NO: 2061
THBS1	NM_003246.1	Forward Primer	CATCCGCAAAGTGACTGAAGAG	SEQ ID NO: 2062
		Probe	CCAATGAGCTGAGGCGGCCTCC	SEQ ID NO: 2063
		Reverse Primer	GTACTGAACTCCGTTGTGATAGCATAG	SEQ ID NO: 2064
THY1	NM_006288.2	Forward Primer	GGACAAGACCCTCTCAGGCT	SEQ ID NO: 2065
		Probe	CAAGCTCCCAAGAGCTTCCAGAGC	SEQ ID NO: 2066
		Reverse Primer	TTGGAGGCTGTGGGTCAG	SEQ ID NO: 2067
TIMP1	NM_003254.1	Forward Primer	TCCCTGCGGTCCCAGATAG	SEQ ID NO: 2068
		Probe	ATCCTGCCCGGAGTGGAACTGAAGC	SEQ ID NO: 2069
		Reverse Primer	GTGGGAACAGGGTGGACACT	SEQ ID NO: 2070
TIMP2	NM_003255.2	Forward Primer	TCACCCTCTGTGACTTCATCGT	SEQ ID NO: 2071
		Probe	CCCTGGGACACCCTGAGCACCA	SEQ ID NO: 2072
		Reverse Primer	TGTGGTTCAGGCTCTTCTTCTG	SEQ ID NO: 2073
TIMP3	NM_000362.2	Forward Primer	CTACCTGCCTTGCTTTGTGA	SEQ ID NO: 2074
		Probe	CCAAGAACGAGTGTCTCTGGACCG	SEQ ID NO: 2075
		Reverse Primer	ACCGAAATTGGAGAGCATGT	SEQ ID NO: 2076
TJP1	NM_003257.1	Forward Primer	ACTTTGCTGGGACAAAGGTC	SEQ ID NO: 2077
		Probe	CTCGGGCCTGCCCACTTCTTC	SEQ ID NO: 2078
		Reverse Primer	CACATGGACTCCTCAGCATC	SEQ ID NO: 2079
TK1	NM_003258.1	Forward Primer	GCCGGGAAGACCGTAATTGT	SEQ ID NO: 2080
		Probe	CAAATGGCTTCCTCTGGAAGGTCCCA	SEQ ID NO: 2081
		Reverse Primer	CAGCGGCACCAGGTTCAG	SEQ ID NO: 2082
TLN1	NM_006289.2	Forward Primer	AAGCAGAAGGGAGAGCGTAAGA	SEQ ID NO: 2083
		Probe	CTTCCAGGCACACAAGAATTGTGGGC	SEQ ID NO: 2084
		Reverse Primer	CCTTGGCCTCAATCTCACTCA	SEQ ID NO: 2085
TMEPAI	NM_020182.3	Forward Primer	CAGAAGGATGCCTGTGGC	SEQ ID NO: 2086
		Probe	ATTCCGTTGCCTGACACTGTGCTC	SEQ ID NO: 2087
		Reverse Primer	GTAGACCTGCGGCTCTGG	SEQ ID NO: 2088
TMSB10	NM_021103.2	Forward Primer	GAAATCGCCAGCTTCGATAA	SEQ ID NO: 2089
		Probe	CGTCTCCGTTTTCTTCAGCTTGGC	SEQ ID NO: 2090
		Reverse Primer	GTCGGCAGGGTGTTCTTTT	SEQ ID NO: 2091
TMSB4X	NM_021109.2	Forward Primer	CACATCAAAGAACTACTGACAACGAA	SEQ ID NO: 2092
		Probe	CCGCGCCTGCCTTTCCCA	SEQ ID NO: 2093
		Reverse Primer	CCTGCCAGCCAGATAGATAGACA	SEQ ID NO: 2094
TNC	NM_002160.1	Forward Primer	AGCTCGGAACCTCACCGT	SEQ ID NO: 2095
		Probe	CAGCCTTCGGGCTGTGGACATAC	SEQ ID NO: 2096
		Reverse Primer	GTAGCAGCCTTGAGGCCC	SEQ ID NO: 2097
TNF	NM_000594.1	Forward Primer	GGAGAAGGGTGACCGACTCA	SEQ ID NO: 2098
		Probe	CGCTGAGATCAATCGGCCCGACTA	SEQ ID NO: 2099
		Reverse Primer	TGCCCAGACTCGGCAAAG	SEQ ID NO: 2100
TNFRSF5	NM_001250.3	Forward Primer	TCTCACCTCGCTATGGTTCGT	SEQ ID NO: 2101
		Probe	TGCCTCTGCAGTGCGTCCTCTGG	SEQ ID NO: 2102
		Reverse Primer	GATGGACAGCGGTCAGCAA	SEQ ID NO: 2103
TNFRSF6B	NM_003823.2	Forward Primer	CCTCAGCACCAGGGTACCA	SEQ ID NO: 2104
		Probe	TGACGGCACGCTCACACTCCTCAG	SEQ ID NO: 2105
		Reverse Primer	TGTCCTGGAAAGCCACAAAGT	SEQ ID NO: 2106

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
TNFSF4	NM_003326.2	Forward Primer	CTTCATCTTCCCTCTACCCAGA	SEQ ID NO: 2107
		Probe	CAGGGGTTGGACCCTTTCCATCTT	SEQ ID NO: 2108
		Reverse Primer	GCTGCATTTCCCACATTCTC	SEQ ID NO: 2109
TOP2A	NM_001067.1	Forward Primer	AATCCAAGGGGGAGAGTGAT	SEQ ID NO: 2110
		Probe	CATATGGACTTTGACTCAGCTGTGGC	SEQ ID NO: 2111
		Reverse Primer	GTACAGATTTTGCCCGAGGA	SEQ ID NO: 2112
TOP2B	NM_001068.1	Forward Primer	TGTGGACATCTTCCCCTCAGA	SEQ ID NO: 2113
		Probe	TTCCCTACTGAGCCACCTTCTCTG	SEQ ID NO: 2114
		Reverse Primer	CTAGCCCGACCGGTTCGT	SEQ ID NO: 2115
TP	NM_001953.2	Forward Primer	CTATATGCAGCCAGAGATGTGACA	SEQ ID NO: 2116
		Probe	ACAGCCTGCCACTCATCACAGCC	SEQ ID NO: 2117
		Reverse Primer	CCACGAGTTTCTTACTGAGAATGG	SEQ ID NO: 2118
TP53BP1	NM_005657.1	Forward Primer	TGCTGTTGCTGAGTCTGTTG	SEQ ID NO: 2119
		Probe	CCAGTCCCCAGAAGACCATGTCTG	SEQ ID NO: 2120
		Reverse Primer	CTTGCCTGGCTTCACAGATA	SEQ ID NO: 2121
TP53BP2	NM_005426.1	Forward Primer	GGGCCAAATATTCAGAAGC	SEQ ID NO: 2122
		Probe	CCACCATAGCGGCCATGGAG	SEQ ID NO: 2123
		Reverse Primer	GGATGGGTATGATGGGACAG	SEQ ID NO: 2124
TP53I3	NM_004881.2	Forward Primer	GCGGACTTAATGCAGAGACA	SEQ ID NO: 2125
		Probe	CAGTATGACCCACCTCCAGGAGCC	SEQ ID NO: 2126
		Reverse Primer	TCAAGTCCCAAAATGTTGCT	SEQ ID NO: 2127
TRAG3	NM_004909.1	Forward Primer	GACGCTGGTCTGGTGAAGATG	SEQ ID NO: 2128
		Probe	CCAGGAAACCACGAGCCTCCAGC	SEQ ID NO: 2129
		Reverse Primer	TGGGTGGTTGTTGGACAATG	SEQ ID NO: 2130
TRAIL	NM_003810.1	Forward Primer	CTTCACAGTGCTCCTGCAGTCT	SEQ ID NO: 2131
		Probe	AAGTACACGTAAGTTACAGCCACACA	SEQ ID NO: 2132
		Reverse Primer	CATCTGCTTCAGCTCGTTGGT	SEQ ID NO: 2133
TS	NM_001071.1	Forward Primer	GCCTCGGTGTGCCTTTCA	SEQ ID NO: 2134
		Probe	CATCGCCAGCTACGCCCTGCTC	SEQ ID NO: 2135
		Reverse Primer	CGTGATGTGCGCAATCATG	SEQ ID NO: 2136
TST	NM_003312.4	Forward Primer	GGAGCCGGATGCAGTAGGA	SEQ ID NO: 2137
		Probe	ACCACGGATATGGCCCGAGTCCA	SEQ ID NO: 2138
		Reverse Primer	AAGTCCATGAAAGGCATGTTGA	SEQ ID NO: 2139
TUBA1	NM_006000.1	Forward Primer	TGTCACCCCGACTCAACGT	SEQ ID NO: 2140
		Probe	AGACGCACCGCCCGGACTCAC	SEQ ID NO: 2141
		Reverse Primer	ACGTGGACTGAGATGCATTCAC	SEQ ID NO: 2142
TUBB	NM_001069.1	Forward Primer	CGAGGACGAGGCTTAAAAAC	SEQ ID NO: 2143
		Probe	TCTCAGATCAATCGTGCATCCTTAGTGAA	SEQ ID NO: 2144
		Reverse Primer	ACCATGCTTGAGGACAACAG	SEQ ID NO: 2145
TUFM	NM_003321.3	Forward Primer	GTATCACCATCAATGCGGC	SEQ ID NO: 2146
		Probe	CATGTGGAGTATAGCACTGCCGCC	SEQ ID NO: 2147
		Reverse Primer	CAGTCTGTGTGGGCGTAGTG	SEQ ID NO: 2148
TULP3	NM_003324.2	Forward Primer	TGTGTATAGTCCTGCCCCTCAA	SEQ ID NO: 2149
		Probe	CCGGATTATCCGACATCTTACTGTGA	SEQ ID NO: 2150
		Reverse Primer	CCCGATCCATTCCCCTTTTA	SEQ ID NO: 2151
tusc4	NM_006545.4	Forward Primer	GGAGGAGCTAAATGCCTCAG	SEQ ID NO: 2152
		Probe	ACTCATCAATGGGCAGAGTGCACC	SEQ ID NO: 2153
		Reverse Primer	CCTTCAAGTGGATGGTGTTG	SEQ ID NO: 2154
UBB	NM_018955.1	Forward Primer	GAGTCGACCCTGCACCTG	SEQ ID NO: 2155
		Probe	AATTAACAGCCACCCCTCAGGCG	SEQ ID NO: 2156
		Reverse Primer	GCGAATGCCATGACTGAA	SEQ ID NO: 2157
UBC	NM_021009.2	Forward Primer	ACGCACCCTGTCTGACTACA	SEQ ID NO: 2158
		Probe	CATCCAGAAAGAGTCCACCCTGCA	SEQ ID NO: 2159
		Reverse Primer	ACCTCTAAGACGGAGCACCA	SEQ ID NO: 2160
UBE2C	NM_007019.2	Forward Primer	TGTCTGGCGATAAAGGGATT	SEQ ID NO: 2161
		Probe	TCTGCCTTCCCTGAATCAGACAACC	SEQ ID NO: 2162
		Reverse Primer	ATGGTCCCTACCCATTTGAA	SEQ ID NO: 2163

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
UBE2M	NM_003969.1	Forward Primer	CTCCATAATTTATGGCCTGCAGTA	SEQ ID NO: 2164
		Probe	TCTTCTTGGAGCCCAACCCCGAG	SEQ ID NO: 2165
		Reverse Primer	TGCGGCCTCCTTGTTCAG	SEQ ID NO: 2166
UBL1	NM_003352.3	Forward Primer	GTGAAGCCACCGTCATCATG	SEQ ID NO: 2167
		Probe	CTGACCAGGAGGCAAAACCTTCAACTGA	SEQ ID NO: 2168
		Reverse Primer	CCTTCCTTCTTATCCCCCAAGT	SEQ ID NO: 2169
UCP2	NM_003355.2	Forward Primer	ACCATGCTCCAGAAGGAGG	SEQ ID NO: 2170
		Probe	CCCCGAGCCTTCTACAAAGGGTTC	SEQ ID NO: 2171
		Reverse Primer	AACCCAAGCGGAGAAAGG	SEQ ID NO: 2172
UGT1A1	NM_000463.2	Forward Primer	CCATGCAGCCTGGAATTTG	SEQ ID NO: 2173
		Probe	CTACCCAGTGCCCCAACCCATTCTC	SEQ ID NO: 2174
		Reverse Primer	GAGAGGCCTGGGCACGTA	SEQ ID NO: 2175
UMPS	NM_000373.1	Forward Primer	TGCGGAAATGAGCTCCAC	SEQ ID NO: 2176
		Probe	CCCTGGCCACTGGGGACTACACTA	SEQ ID NO: 2177
		Reverse Primer	CCTCAGCCATTCTAACCGC	SEQ ID NO: 2178
UNC5A	XM_030300.7	Forward Primer	GACAGCTGATCCAGGAGCC	SEQ ID NO: 2179
		Probe	CGGGTCCTGCACTTCAAGGACAGT	SEQ ID NO: 2180
		Reverse Primer	ATGGATAGGCGCAGGTTG	SEQ ID NO: 2181
UNC5B	NM_170744.2	Forward Primer	AGAACGGAGGCCGTGACT	SEQ ID NO: 2182
		Probe	CGGGACGCTGCTCGACTCTAAGAA	SEQ ID NO: 2183
		Reverse Primer	CATGCACAGCCCATCTGT	SEQ ID NO: 2184
UNC5C	NM_003728.2	Forward Primer	CTGAACACAGTGGAGCTGGT	SEQ ID NO: 2185
		Probe	ACCTGCCGCACACAGAGTTTGC	SEQ ID NO: 2186
		Reverse Primer	CTGGAAGATCTGCCCTTCTC	SEQ ID NO: 2187
upa	NM_002658.1	Forward Primer	GTGGATGTGCCCTGAAGGA	SEQ ID NO: 2188
		Probe	AAGCCAGGCGTCTACACGAGAGTCTCAC	SEQ ID NO: 2189
		Reverse Primer	CTGCGGATCCAGGGTAAGAA	SEQ ID NO: 2190
UPP1	NM_003364.2	Forward Primer	ACGGGTCCTGCCTCAGTT	SEQ ID NO: 2191
		Probe	TCAGCTTTCTCTGCATTGGCTCCC	SEQ ID NO: 2192
		Reverse Primer	CGGGGCAATCATTGTGAC	SEQ ID NO: 2193
VCAM1	NM_001078.2	Forward Primer	TGGCTTCAGGAGCTGAATACC	SEQ ID NO: 2194
		Probe	CAGGCACACACAGGTGGGACACAAAT	SEQ ID NO: 2195
		Reverse Primer	TGCTGTCGTGATGAGAAAATAGTG	SEQ ID NO: 2196
VCL	NM_003373.2	Forward Primer	GATACCACAACTCCCATCAAGCT	SEQ ID NO: 2197
		Probe	AGTGGCAGCCACGGCGCC	SEQ ID NO: 2198
		Reverse Primer	TCCCTGTTAGGCGCATCAG	SEQ ID NO: 2199
VCP	NM_007126.2	Forward Primer	GGCTTTGGCAGCTTCAGAT	SEQ ID NO: 2200
		Probe	AGCTCCACCCTGGTTCCCTGAAG	SEQ ID NO: 2201
		Reverse Primer	CTCCACTGCCCTGACTGG	SEQ ID NO: 2202
VDAC1	NM_003374.1	Forward Primer	GCTGCGACATGGATTTCGA	SEQ ID NO: 2203
		Probe	TTGCTGGGCCTTCCATCCGG	SEQ ID NO: 2204
		Reverse Primer	CCAGCCCTCGTAACCTAGCA	SEQ ID NO: 2205
VDAC2	NM_003375.2	Forward Primer	ACCCACGGACAGACTTGC	SEQ ID NO: 2206
		Probe	CGCGTCCAATGTGTATTCCTCCAT	SEQ ID NO: 2207
		Reverse Primer	AGCTTTGCCAAGGTCAGC	SEQ ID NO: 2208
VDR	NM_000376.1	Forward Primer	GCCCTGGATTTCAGAAAGAG	SEQ ID NO: 2209
		Probe	CAAGTCTGGATCTGGGACCCTTTCC	SEQ ID NO: 2210
		Reverse Primer	AGTTACAAGCCAGGGAAGGA	SEQ ID NO: 2211
VEGF	NM_003376.3	Forward Primer	CTGCTGTCTTGGGTGCATTG	SEQ ID NO: 2212
		Probe	TTGCCTTGCTGCTCTACCTCCACCA	SEQ ID NO: 2213
		Reverse Primer	GCAGCCTGGGACCACTTG	SEQ ID NO: 2214
VEGF_altsplice1	AF486837.1	Forward Primer	TGTGAATGCAGACCAAAGAAAGA	SEQ ID NO: 2215
		Probe	AGAGCAAGACAAGAAAATCCCTGTGGGC	SEQ ID NO: 2216
		Reverse Primer	GCTTTCTCCGCTCTGAGCAA	SEQ ID NO: 2217
VEGF_altsplice2	AF214570.1	Forward Primer	AGCTTCCTACAGCACAACAAAT	SEQ ID NO: 2218
		Probe	TGTCTTGCTCTATCTTTCTTTGGTCTGCA	SEQ ID NO: 2219
		Reverse Primer	CTCGGCTTGTCACATTTTTC	SEQ ID NO: 2220

TABLE A-continued

Gene	Accession	Reagent	Sequence	Sequence ID Number
VEGFB	NM_003377.2	Forward Primer	TGACGATGGCCTGGAGTGT	SEQ ID NO: 2221
		Probe	CTGGGCAGCACCAAGTCCGGA	SEQ ID NO: 2222
		Reverse Primer	GGTACCGGATCATGAGGATCTG	SEQ ID NO: 2223
VEGFC	NM_005429.2	Forward Primer	CCTCAGCAAGACGTTATTTGAAATT	SEQ ID NO: 2224
		Probe	CCTCTCTCTCAAGGCCCCAAACCAGT	SEQ ID NO: 2225
		Reverse Primer	AAGTGTGATTGGCAAAACTGATTG	SEQ ID NO: 2226
VIM	NM_003380.1	Forward Primer	TGCCCTTAAAGGAACCAATGA	SEQ ID NO: 2227
		Probe	ATTTCACGCATCTGGCGTTCCA	SEQ ID NO: 2228
		Reverse Primer	GCTTCAACGGCAAAGTTCTCTT	SEQ ID NO: 2229
WIF	NM_007191.2	Forward Primer	TACAAGCTGAGTGCCCAGG	SEQ ID NO: 2230
		Probe	TACAAAAGCCTCCATTTCGGCACC	SEQ ID NO: 2231
		Reverse Primer	CACTCGCAGATGCGTCTTT	SEQ ID NO: 2232
WISP1	NM_003882.2	Forward Primer	AGAGGCATCCATGAACTTCACA	SEQ ID NO: 2233
		Probe	CGGGCTGCATCAGCACACGC	SEQ ID NO: 2234
		Reverse Primer	CAAACTCCACAGTACTTGGGTTGA	SEQ ID NO: 2235
Wnt-3a	NM_033131.2	Forward Primer	ACAAAGCTACCAGGGAGTCG	SEQ ID NO: 2236
		Probe	TTTGTCCACGCCATTGCCTCAG	SEQ ID NO: 2237
		Reverse Primer	TGAGCGTGTCACTGCAAAG	SEQ ID NO: 2238
Wnt-5a	NM_003392.2	Forward Primer	GTATCAGGACCACATGCAGTACATC	SEQ ID NO: 2239
		Probe	TTGATGCCTGTCTTCGCGCCTTCT	SEQ ID NO: 2240
		Reverse Primer	TGTCGGAATTGATACTGGCATT	SEQ ID NO: 2241
Wnt-5b	NM_032642.2	Forward Primer	TGTCTTCAGGGTCTTGTCCA	SEQ ID NO: 2242
		Probe	TTCCGTAAGAGGCCTGGTGCTCTC	SEQ ID NO: 2243
		Reverse Primer	GTGCACGTGGATGAAAGAGT	SEQ ID NO: 2244
WNT2	NM_003391.1	Forward Primer	CGGTGGAATCTGGCTCTG	SEQ ID NO: 2245
		Probe	CTCCCTCTGCTCTTGACCTGGCTC	SEQ ID NO: 2246
		Reverse Primer	CCATGAAGAGTTGACCTCGG	SEQ ID NO: 2247
WWOX	NM_016373.1	Forward Primer	ATCGCAGCTGGTGGGTGTA	SEQ ID NO: 2248
		Probe	CTGCTGTTTACCTTGGCGAGGCCTTT	SEQ ID NO: 2249
		Reverse Primer	AGCTCCCTGTTGCATGGACTT	SEQ ID NO: 2250
XPA	NM_000380.2	Forward Primer	GGGTAGAGGGAAAAGGGTTC	SEQ ID NO: 2251
		Probe	CAAAGGCTGAACTGGATTCTTAACCAAGA	SEQ ID NO: 2252
		Reverse Primer	TGCACCACCATTGCTATTATT	SEQ ID NO: 2253
XPC	NM_004628.2	Forward Primer	GATACATCGTCTGCGAGGAA	SEQ ID NO: 2254
		Probe	TTCAAAGACGTGCTCCTGACTGCC	SEQ ID NO: 2255
		Reverse Primer	CTTTCAATGACTGCCTGCTC	SEQ ID NO: 2256
XRCC1	NM_006297.1	Forward Primer	GGAGATGAAGCCCCCAAG	SEQ ID NO: 2257
		Probe	AGAAGCAACCCCAGACCAAAACCA	SEQ ID NO: 2258
		Reverse Primer	GTCCAGCTGCCTGAGTGG	SEQ ID NO: 2259
YB-1	NM_004559.1	Forward Primer	AGACTGTGGAGTTTGATGTTGTTGA	SEQ ID NO: 2260
		Probe	TTGCTGCCTCCGCACCCTTTTCT	SEQ ID NO: 2261
		Reverse Primer	GGAACACCACCAGGACCTGTAA	SEQ ID NO: 2262
YWHAH	NM_003405.2	Forward Primer	CATGGCCTCCGCTATGAA	SEQ ID NO: 2263
		Probe	AGGTTCATTCAGCTCTGTCACCGC	SEQ ID NO: 2264
		Reverse Primer	GGAGATTTCGATCTTCATTGGA	SEQ ID NO: 2265
zbtb7	NM_015898.2	Forward Primer	CTGCGTTCACACCCCAGT	SEQ ID NO: 2266
		Probe	TCTCTCCAGAACAGCTCGCCCTGT	SEQ ID NO: 2267
		Reverse Primer	CTCAGCCACGACAGATGGT	SEQ ID NO: 2268
ZG16	NM_152338.1	Forward Primer	TGCTGAGCCTCCTCTCCTT	SEQ ID NO: 2269
		Probe	TACTCCTCATCACAGTGCCCCTGC	SEQ ID NO: 2270
		Reverse Primer	GGATGGGGGTTAGTGATAAGG	SEQ ID NO: 2271

TABLE B

Gene	Locus Link	Sequence	Sequence ID Number
A-Catenin	NM_001903.1	CGTTCCGATCCTCTATACTGCATCCCAGGCATGCCTACAGCACCCTGATGTCGCAGCCTATAAGGCCAACAGGGACCT	SEQ ID NO: 2272
ABCB1	NM_000927.2	AAACACCACTGGAGCATTGACTACCAGGCTCGCCAATGATGCTGCTCAAGTTAAAGGGGCTATAGGTTCCAGGCTTG	SEQ ID NO: 2273
ABCC5	NM_005688.1	TGCAGACTGTACCATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTGGCC	SEQ ID NO: 2274
ABCC6	NM_001171.2	GGATGAACCTCGACCTGCTGCAGGAGCACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTC	SEQ ID NO: 2275
ACP1	NM_004300.2	GCTACCAAGTCCGTGCTGTTTGTGTGTCTGGGTAACATTTGTCGATCACCCATTGCAGAAGCAGTTTTC	SEQ ID NO: 2276
ADAM10	NM_001110.1	CCCATCAACTTGTGCCAGTACAGGGTCTGTGCAGTGGAGTAGGCACTTCAGTGGTCGAACCATCACC	SEQ ID NO: 2277
ADAM17	NM_003183.3	GAAGTGCCAGGAGGCGATTAATGCTACTTGCAAAGGCGTGTCCTACTGCACAGGTAATAGCAGTGAGTGCCCG	SEQ ID NO: 2278
ADAMTS12	NM_030955.2	GGAGAAGGGTGGAGTGCAGCACCCAGATGGATTCTGACTGTGCGGCCATCCAGAGACCTGACCCTG	SEQ ID NO: 2279
ADPRT	NM_001618.2	TTGACAACCTGCTGGACATCGAGGTGGCCTACAGTCTGCTCAGGGGAGGGTCTGATGATAGCAGCAAGGATCCCAT	SEQ ID NO: 2280
AGXT	NM_000030.1	CTTTTCCCTCCAGTGGCACCTCCTGGAAACAGTCCACTTGGGCGCAAAACCCAGTGCCTTCCAAAT	SEQ ID NO: 2281
AKAP12	NM_005100.2	TAGAGAGCCCCTGACAATCCTGAGGCTTCATCAGGAGCTAGAGCCATTTAACATTTCCTCTTTCCAAGACCAACC	SEQ ID NO: 2282
AKT1	NM_005163.1	CGCTTCTATGGCGCTGAGATTGTGTCAGCCCTGGACTACCTGCACTCGGAGAAGAACGTGGTGTACCGGGA	SEQ ID NO: 2283
AKD2	NM_001626.2	TCCTGCCACCCTTCAAACCTCAGGTCACGTCCGAGGTCGACACAAGGTACTTCGATGATGAATTTACCGCC	SEQ ID NO: 2284
AKT3	NM_005465.1	TTGTCTGTGCCTTGGACTATCTACATTCCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGAATCTAATGCTGG	SEQ ID NO: 2285
AL137428	AL137428.1	CAAGAAGAGGCTCTACCCTGGGACTGGGAATTTCCAAGGCCACCTTTGAGGATCGCAGAGCTCATTT	SEQ ID NO: 2286
ALCAM	NM_001627.1	GAGGAATATGGAATCCAAGGGGGCCAGTTCCTGCCGTCTGCTCTTCTGCCTCTTGATCTCCGCCAC	SEQ ID NO: 2287
ALDH1A1	NM_000689.1	GAAGGAGATAAGGAGGATGTTGACAAGGCAGTGAAGGCCGCAAGACAGGCTTTTCAGATTGGATCTCCGTGGCG	SEQ ID NO: 2288
ALDOA	NM_000034.2	GCCTGTACGTGCCAGCTCCCCGACTGCCAGAGCCTCAACTGTCTCTGCTTCGAGATCAAGCTCCGATGA	SEQ ID NO: 2289
AMFR	NM_001144.2	GATGGTTCAGCTCTGCAAGGATCGATTTGAATATCTTTCCTTCTCGCCCACCACGCCGATGAGCAGCCACGGTCGA	SEQ ID NO: 2290
ANGPD2	NM_001147.1	CCGTGAAAGCTGCTCTGTAAAAGCTGACACAGCCCTCCCAAGTGAGCAGGACTGTTCTTCCCACTGCAA	SEQ ID NO: 2291
ANTXR1	NM_032208.1	CTCCAGGTGTACCTCCAACCCTAGCCTTCTCCCACAGCTGCCTACAACAGAGTCTCCCAGCCTTCTC	SEQ ID NO: 2292
ANXA1	NM_000700.1	GCCCCTATCCTACCTTCAATCCATCCTCGGATGTCGCTGCCTTGCATAAGGCCATAATGGTTAAAGG	SEQ ID NO: 2293
ANXA2	NM_004039.1	CAAGACACTAAGGGCGACTACCAGAAAGCGCTGCTGTACCTGTGTGGTGGAGATGACTGAAGCCCGACACG	SEQ ID NO: 2294
ANXA5	NM_001154.2	GCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCT	SEQ ID NO: 2295
AP-1 (JUN official)	NM_002228.2	GACTGCAAAGATGGAAACGACCTTCTATGACGATGCCCTCAACGCCTCGTTCCTCCCGTCCGAGAGCGGACCTTATGGCTA	SEQ ID NO: 2296

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
APC	NM_000038.1	GGACAGCAGGAATGTGTTTCTCCATACAGGTCACGGGGAGCCAATGGTTCAGAAACAAATCGAGTGGGT	SEQ ID NO: 2297
APEX-1	NM_001641.2	GATGAAGCCTTTCGCAAGTTCCTGAAGGGCCTGGCTTCCCGAAAGCCCCTTGTGCTGTGTGGAGACCT	SEQ ID NO: 2298
APG-1	NM_014278.2	ACCCCGGCCTGTATATCATTGGGATCAAGAACTCGAGCCATTGGAAATGCAGCAAAGAGCCAGATAG	SEQ ID NO: 2299
APN (ANPEP official)	NM_001150.1	CCACCTTGGACCAAAGTAAAGCGTGGAATCGTTACCGCCTCCCCAACACGCTGAAACCCGATTCCTACCAGGTGACGCTGAGA	SEQ ID NO: 2300
APOC1	NM_001645.3	GGAAACACACTGGAGGACAAGGCTCGGGAACTCATCAGCCGCATCAAACAGAGTGAACTTTCTGCCAAGATGCG	SEQ ID NO: 2301
AREG	NM_001657.1	TGTGAGTGAAATGCCTTCTAGTAGTGAACCGTCCTCGGGAGCCGACTATGACTACTCAGAAGAGTATGATAACGAACCACAA	SEQ ID NO: 2302
ARG	NM_005158.2	CGCAGTGCAGCTGAGTATCTGCTCAGCAGTCTAATCAATGGCAGCTTCCTGGTGCGAGAAAGTGAGAGTAGCCCTGGGCA	SEQ ID NO: 2303
ARHF	NM_019034.2	ACTGGCCCACTTAGTCCTCAAGCTCCCAACCTGCTGTCCCTCAAGCCCCGCTTCTACCAGCCTGTGGAGTTCAG	SEQ ID NO: 2304
ATOH1	NM_005172.1	GCAGCCACCTGCAACTTTGCAGGCGAGAGAGCATCCCGTCTACCCGCCTGAGCTGTCCCTCCTGGA	SEQ ID NO: 2305
ATP5A1	NM_004046.3	GATGCTGCCACTCAACAACTTTTGAGTCGTGGCGTGCGTCTAACTGAGTTGCTGAAGCAAGGACA	SEQ ID NO: 2306
ATP5E	NM_006886.2	CCGCTTTCGCTACAGCATGGTGGCCTACTGGAGACAGGCTGGACTCAGCTACATCCGATACTCCCA	SEQ ID NO: 2307
AURKB	NM_004217.1	AGCTGCAGAAGAGCTGCACATTTGACGAGCAGCGAACAGCCACGATCATGGAGGAGTTGGCAGATGC	SEQ ID NO: 2308
Axin 2	NM_004655.2	GGCTATGTCTTTGCACCAGCCACCAGCGCCAACGACAGTGAGATATCCAGTGATGCGCTGACGGAT	SEQ ID NO: 2309
axin1	NM_003502.2	CCGTGTGACAGCATCGTTGTGGCGTACTACTTCTGCGGGGAACCCATCCCCTACCGCACCCTGGTGAG	SEQ ID NO: 2310
B-Catenin	NM_001904.1	GGCTCTTGTGCGTACTGTCCTTCGGGCTGGTGACAGGGAAGACATCACTGAGCCTGCCATCTGTGCTCTTCGTCATCTGA	SEQ ID NO: 2311
BAD	NM_032989.1	GGGTCAGGTGCCTCGAGATCGGGCTTGGGCCCAGAGCATGTTCCAGATCCCAGAGTTTGAGCCGAGTGAGCAG	SEQ ID NO: 2312
BAG1	NM_004323.2	CGTTGTCAGCACTTGGAATACAAGATGGTTGCCGGGTCATGTTAATTGGGAAAAAGAACAGTCCACAGGAAGAGGTTGAAC	SEQ ID NO: 2313
BAG2	NM_004282.2	CTAGGGGCAAAAAGCATGACTGCTTTTTCCTGTCTGGCATGGAATCACGCAGTCACCTTGGGCATTTAG	SEQ ID NO: 2314
BAG3	NM_004281.2	GAAAGTAAGCCAGGCCCAGTTGGACCAGAACTCCCTCCTGGACACATCCCAATTCAAGTGATCCGCAAAGAGGT	SEQ ID NO: 2315
Bak	NM_001188.1	CCATTCCCACCATTCTACCTGAGGCCAGGACGTCTGGGGTGTGGGGATTGGTGGGTCTATGTTCCC	SEQ ID NO: 2316
Bax	NM_004324.1	CCGCCGTGGACACAGACTCCCCCCGAGAGGTCTTTTTCCGAGTGGCAGCTGACATGTTTTCTGACGGCAA	SEQ ID NO: 2317
BBC3	NM_014417.1	CCTGGAGGGTCCTGTACAATCTCATCATGGGACTCCTGCCCTTACCCAGGGGCCACAGAGCCCCCGAGATGGAGCCCAATTAG	SEQ ID NO: 2318
BCAS1	NM_003657.1	CCCCGAGACAACGGAGATAAGTGCTGTTGCGGATGCCAACGGAAAGAATCTTGGGAAAGAGGCCAAACCCGAG	SEQ ID NO: 2319
Bcl2	NM_000633.1	CAGATGGACCTAGTACCCACTGAGATTTCCACGCCGAAGGACAGCGATGGGAAAAATGCCCTTAAATCATAGG	SEQ ID NO: 2320
BCL2L10	NM_020396.2	GCTGGGATGGCTTTTGTCACTTCTTCAGGACCCCCTTTCCACTGGCTTTTTGGAGAAAACAGCTGGTCCAGGC	SEQ ID NO: 2321

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
BCL2L11	NM_138621.1	AATTACCAAGCAGCCGAAGACCACCCACGAATGGTTATCTTACGACTGTTACGTTACATTGTCCGCCTG	SEQ ID NO: 2322
BCL2L12	NM_138639.1	AACCCACCCCTGTCTTGGAGCTCCGGGTAGCTCTCAAACTCGAGGCTGCGCACCCCCTTTCCCGTCAGCTGAG	SEQ ID NO: 2323
Bclx	NM_001191.1	CTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTG	SEQ ID NO: 2324
BCRP	NM_004827.1	TGTACTGGCGAAGAATATTTGGTAAAGCAGGGCATCGATCTCTCACCCTGGGGCTTGTGGAAGAATCACGTGGC	SEQ ID NO: 2325
BFGF	NM_007083.1	CCAGGAAGAATGCTTAAGATGTGAGTGGATGGATCTCAATGACCTGGCGAAGACTGAAAATACAACTCCCATCACCA	SEQ ID NO: 2326
BGN	NM_001711.3	GAGCTCCGCAAGGATGACTTCAAGGGTCTCCAGCACCTCTACGCCCTCGTCCTGGTGAACAACAAG	SEQ ID NO: 2327
BID	NM_001196.2	GGACTGTGAGGTCAACAACGGTTCCAGCCTCAGGGATGAGTGCATCACAAACCTACTGGTGTTTGGCTTCC	SEQ ID NO: 2328
BIK	NM_001197.3	ATTCCTATGGCTCTGCAATTGTCACCGGTTAACTGTGGCCTGTGCCCAGGAAGAGCCATTCACTCCTGCC	SEQ ID NO: 2329
BIN1	NM_004305.1	CCTGCAAAAGGGAACAAGAGCCCTTCGCCTCCAGATGGCTCCCCTGCCGCCACCCCCGAGATCAGAGTCAACCACG	SEQ ID NO: 2330
BLMH	NM_000386.2	GGTTGCTGCCTCCATCAAAGATGGAGAGGCTGTGTGGTTTGGCTGTGATGTTGGAAAACACTTCAATAGCAAGCTGG	SEQ ID NO: 2331
BMP2	NM_001200.1	ATGTGGACGCTCTTTCAATGGACGTGTCCCCGCGTGCTTCTTAGACGGACTGCGGTCTCCTAAAGGTCGACCATGGT	SEQ ID NO: 2332
BMP4	NM_001202.2	GGGCTAGCCATTGAGGTGACTCACCTCCATCAGACTCGGACCCACCAGGGCCAGCATGTCAGGATTAGC	SEQ ID NO: 2333
BMP7	NM_001719.1	TCGTGGAACATGACAAGGAATTCTTCCACCCACGCTACCACCATCGAGAGTTCCGGTTTGATCTTTCCA	SEQ ID NO: 2334
BMPR1A	NM_004329.2	TTGGTTCAGCGAACTATTGCCAAACAGATTCAGATGGTCCGGCAAGTTGGTAAAGGCCGATATGGAGA	SEQ ID NO: 2335
BRAF	NM_004333.1	CCTTCCGACCAGCAGATGAAGATCATCGAAATCAATTTGGGCAACGAGACCGATCCTCATCAGCTCCCAATGTGCATATAAA	SEQ ID NO: 2336
BRCA1	NM_007295.1	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCACCAACATGCCCACAGATCAACTGGAATGG	SEQ ID NO: 2337
BRCA2	NM_000059.1	AGTTCGTGCTTTGCAAGATGGTGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAGACCCAGCTTACCTT	SEQ ID NO: 2338
BRK	NM_005975.1	GTGCAGGAAAGGTTCACAAATGTGGAGTGTCTGCGTCCAATACACGCGTGTGCTCCTCTCCTTACTCCATCGTGTGTGC	SEQ ID NO: 2339
BTF3	NM_001207.2	CAGTGATCCACTTTAACAACCCTAAAGTTCAGGCATCTCTGGCAGCGAACACTTTCACCATTACAGGCCATGCT	SEQ ID NO: 2340
BTRC	NM_033637.2	GTTGGGACACAGTTGGTCTGCAGTCGGCCCAGGACGGTCTACTCAGCACAACTGACTGCTTCA	SEQ ID NO: 2341
BUB1	NM_004336.1	CCGAGGTTAATCCAGCACGTATGGGGCCAAGTGTAGGCTCCCAGCAGGAACTGAGAGCGCCATGTCTT	SEQ ID NO: 2342
BUB1B	NM_001211.3	TCAACAGAAGGCTGAACCACTAGAAAGACTACAGTCCCAGCACCGACAATTCCAAGCTCGAGTGTCTCGGCAAACTCTGTTG	SEQ ID NO: 2343
BUB3	NM_004725.1	CTGAAGCAGATGGTTCATCATTTCCTGGGCTGTTAAACAAAGCGAGGTTAAGGTTAGACTCTTGGGAATCAGC	SEQ ID NO: 2344
c-abl	NM_005157.2	CCATCTCGCTGAGATACGAAGGGAGGGTGTACCATTACAGGATCAACACTGCTTCTGATGGCAAGCTCTACGTCT	SEQ ID NO: 2345
c-kit	NM_000222.1	GAGGCAACTGCTTATGGCTTAATTAAGTCAGATGCGGCCATGACTGTCGCTGTAAAGATGCTCAAGCCGAGTGCC	SEQ ID NO: 2346

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Gene	Locus Link	Sequence	Sequence ID Number
c-myb (MYB official)	NM_005375.1	AACTCAGACTTGGAAATGCCTTCTTTAACTTCCACCCCCCTCATTGGTCACAAATTGACTGTTACAACACCATTTCATAGAGACCAG	SEQ ID NO: 2347
c-Src	NM_005417.3	TGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAG	SEQ ID NO: 2348
C20 orf1	NM_012112.2	TCAGCTGTGAGCTGCGGATACCGCCCGGCAATGGGACCTGCTCTTAACCTCAAACCTAGGACCGT	SEQ ID NO: 2349
C20ORF126	NM_030815.2	CCAGCACTGCTCGTTACTGTCTGCCTTCAGTGGTCTGAGGTCCCAGTATGAACTGCCGTGAAGTCAA	SEQ ID NO: 2350
C8orf4	NM_020130.2	CTACGAGTCAGCCCATCCATCCATGGCTACCACTTCGACACAGCCTCTCGTAAGAAAGCCGTGGGCA	SEQ ID NO: 2351
CA9	NM_001216.1	ATCCTAGCCCTGGTTTTTGGCCTCCTTTTTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGAAGGCAG	SEQ ID NO: 2352
Cad17	NM_004063.2	GAAGGCCAAGAACCGAGTCAAATTATATTCCAGTTTAAGGCCAATCCTCCTGCTGTGACTTTTGAACTAACTGGGGA	SEQ ID NO: 2353
CALD1	NM_004342.4	CACTAAGGTTTGAGACAGTTCCAGAAAGAACCCAAGCTCAAGACGCAGGACGAGCTCAGTTGTAGAGGGCTAATTCGC	SEQ ID NO: 2354
CAPG	NM_001747.1	GATTGTCACTGATGGGGAGGAGCCTGCTGAGATGATCCAGGTCCTGGGCCCCAAGCCTGCTCTGAAGG	SEQ ID NO: 2355
CAPN1	NM_005186.2	CAAGAAGCTGTACGAGCTCATCATCACCCGCTACTCGGAGCCCGACCTGGCGGTCGACTTTGACAATTTCGTTTGCTGC	SEQ ID NO: 2356
CASP8	NM_033357.1	CCTCGGGGATACTGTCTGATCATCAACAATCACAATTTTGCAAAAGCACGGGAGAAAGTGCCCAAACTTC	SEQ ID NO: 2357
CASP9	NM_001229.2	TGAATGCCGTGGATTGCACGTGGCCTCTTGAGCAGTGGCTGGTCCAGGGCTAGTGACTTGTGTCCCATGATCCCTGT	SEQ ID NO: 2358
CAT	NM_001752.1	ATCCATTCGATCTCACCAAGGTTTGGCCTCACAAGGACTACCCTCTCATCCCAGTTGGTAAACTGGTCTTAAACCGGA	SEQ ID NO: 2359
CAV1	NM_001753.3	GTGGCTCAACATTGTGTTCCCATTTCAGCTGATCAGTGGGCCTCCAAGGAGGGGCTGTAAAATGGAGGCCATTG	SEQ ID NO: 2360
CBL	NM_005188.1	TCATTCACAAACCTGGCAGTTATATCTTCCGGCTGAGCTGTACTCGTCTGGGTCAGTGGGCTATTGGGTATG	SEQ ID NO: 2361
CCL20	NM_004591.1	CCATGTGCTGTACCAAGAGTTTGCTCCTGGCTGCTTTGATGTCAGTGCTGCTACTCCACCTCTGCGGCG	SEQ ID NO: 2362
CCL3	NM_002983.1	AGCAGACAGTGGTCAGTCCTTTCTTGGCTCTGCTGACACTCGAGCCCACATTCCGTCACCTGCTCAGAATCATGCAG	SEQ ID NO: 2363
CCNA2	NM_001237.2	CCATACCTCAAGTATTTGCCATCAGTTATTGCTGGAGCTGCCTTTCATTTAGCACTCTACACAGTCACGGGACAAAGCT	SEQ ID NO: 2364
CCNB1	NM_031966.1	TTCAGGTTGTTGCAGGAGACCATGTACATGACTGTCTCCATTATTGATCGGTTCATGCAGAATAATTGTGTGCCCAAGAAGATG	SEQ ID NO: 2365
CCNB2	NM_004701.2	AGGCTTCTGCAGGAGACTCTGTACATGTGCGTTGGCATTATGGATCGATTTTTACAGGTTCAGCCAGTTTCCC	SEQ ID NO: 2366
CCND1	NM_001758.1	GCATGTTCGTGGCCTCTAAGATGAAGGAGACCATCCCCCTGACGGCCGAGAAGCTGTGCATCTACACCG	SEQ ID NO: 2367
CCND3	NM_001760.2	CCTCTGTGCTACAGATTATACCTTTGCCATGTACCCGCCATCCATGATCGCCACGGGCAGCATTGGGGCTGCAGTG	SEQ ID NO: 2368
CCNE1	NM_001238.1	AAAGAAGATGATGACCGGGTTTACCCAAACTCAACGTGCAAGCCTCGGATTATTGCACCATCCAGAGGCTC	SEQ ID NO: 2369
CCNE2	NM_057749.1	ATGCTGTGGCTCCTTCCTAACTGGGGCTTTCTTGACATGTAGGTTGCTTGGTAATAACCTTTTTGTATATCACAATTTGGGT	SEQ ID NO: 2370
CCNE2 variant 1	NM_057749var1	GGTCACCAAGAAACATCAGTATGAAATTAGGAATTGTTGGCCACCTGTATTATCTGGGGGGATCAGTCCTTGCATTATCATTGAA	SEQ ID NO: 2371

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
CCR7	NM_001838.2	GGATGACATGCACTCAGCTCTTGGCTCCACTGGGATG GGAGGAGAGGACAAGGGAAATGTCAGG	SEQ ID NO: 2372
CD105	NM_000118.1	GCAGGTGTCAGCAAGTATGATCAGCAATGAGGCGGTGGT CAATATCCTGTCGAGCTCATCACCACAGCGGAAAAA	SEQ ID NO: 2373
CD134 (TNFRSF4 official)	NM_003327.1	GCCCAGTGCGGAGAACAGGTCCAGCTTGATTCTCGTCTCTGC ACTTAAGCTGTTCTCCAGGTGCGTGTGATT	SEQ ID NO: 2374
CD18	NM_000211.1	CGTCAGGACCCACCATGTCTGCCCCATCACGCGGCCGAGACATG GCTTGGCCACAGCTCTTGAGGATGTCACCAATTAACC	SEQ ID NO: 2375
CD24	NM_013230.1	TCCAACTAATGCCACCACCAAGGCGGCTGGTGGTGCCCTGCAGTCAA CAGCCAGTCTCTTCGTGGTCTCACTCTCTC	SEQ ID NO: 2376
CD28	NM_006139.1	TGTGAAAGGGAAACACCTTTGTCCAAGTCCCCTATTTCCCGGA CCTTCTAAGCCCTTTTGGGTGCT	SEQ ID NO: 2377
CD31	NM_000442.1	TGTATTTCAAGACCTCTGTGCACTTATTTATGAACCTGCCCTGCT CCCACAGAACACAGCAATTCCTCAGGCTAA	SEQ ID NO: 2378
CD34	NM_001773.1	CCACTGCACACACCTCAGAGGCTGTTCTTGGGGCCCTAC ACCTTGAGGAGGGGCAGGTAAACTCCTG	SEQ ID NO: 2379
CD3z	NM_000734.1	AGATGAAGTGGAAGGCGCTTTTCACCGCGGCCATCC TGCAGGCACAGTTGCCGATTACAGAGGCA	SEQ ID NO: 2380
CD44E	X55150	ATCACCGACAGCACAGACAGAATCCCTGCTACCAATATGGACT CCAGTCATAGTACAACGCTTCAGCCTACTGCAAATCCAAACACAGGT	SEQ ID NO: 2381
CD44s	M59040.1	GACGAAGACAGTCCCTGGATCACCGACAGCACAGACAGAATCC CTGCTACCAGAGACCAAGACACATTCCACCCCAGT	SEQ ID NO: 2382
CD44v3	AJ251595v3	CACACAAAACAGAACCAGGACTGGACCCAGTGGAAC CCAAGCCATTCAAATCCGGAAGTGCTACTTCAG	SEQ ID NO: 2383
CD44v6	AJ251595v6	CTCATACCAGCCATCCAATGCAAGGAAGGACAACACCAAGCCCAG AGGACAGTTCCTGGACTGATTTCTTCAACCCAA	SEQ ID NO: 2384
CD68	NM_001251.1	TGGTTCCCAGCCCTGTGTCCACCTCCAAGCCCAGA TTCAGATTCGAGTCATGTACACAACCCAGGGTGGAGGAG	SEQ ID NO: 2385
CD80	NM_005191.2	TTCAGTTGCTTTGCAGGAAGTGTCTAGAGGAAT ATGGTGGGCACAGAAGTAGCTCTGGTGACCTTGATCAA	SEQ ID NO: 2386
CD82	NM_002231.2	GTGCAGGCTCAGGTGAAGTGCTGCGGCTGGGTCAGC TTCTACAACTGGACAGACAACGCTGAGCTCATGAATCGCCCTGAGGTC	SEQ ID NO: 2387
CD8A	NM_171827.1	AGGGTGAGGTGCTTGAGTCTCCAACGGCAAGG GAACAAGTACTTCTTGATACCTGGGATACTGTGCCC	SEQ ID NO: 2388
CD9	NM_001769.1	GGGCGTGGAACAGTTTATCTCAGACATCTGCCCCAAGA AGGACGTACTCGAAACCTTCACCGTG	SEQ ID NO: 2389
CDC2	NM_001786.2	GAGAGCGACGCGGTTGTTGTAGCTGCCGCTGCGGCCGCC GCGGAATAATAAGCCGGGATCTACCATAC	SEQ ID NO: 2390
CDC20	NM_001255.1	TGGATTGGAGTTCTGGGAATGTACTGGCCGTGGCACTGGACA ACAGTGTGTACCTGTGGAGTGCAAGC	SEQ ID NO: 2391
cdc25A	NM_001789.1	TCTTGCTGGCTACGCCTCTTCTGTCCCTGTTAGACGT CCTCCGTCCATATCAGAACTGTGCCACAATGCAG	SEQ ID NO: 2392
CDC25B	NM_021874.1	AAACGAGCAGTTTGCCATCAGACGCTTCCAGTCTATGCCGGT GAGGCTGCTGGGCCACAGCCCCGTGCTTCGGAACATCACCAAC	SEQ ID NO: 2393
CDC25C	NM_001790.2	GGTGAGCAGAAGTGGCCTATATCGCTCCCCGTCGATG CCAGAGAACTTGAACAGGCCAAGACTGAAG	SEQ ID NO: 2394
CDC4	NM_018315.2	GCAGTCCGCTGTGTTCAATATGATGGCAGGAGGGTTGTTA GTGGAGCATATGATTTTATGGTAAAGGTGTGGGATCC	SEQ ID NO: 2395
CDC42	NM_001791.2	TCCAGAGACTGCTGAAAAGCTGGCCCGTGACCTGAAGGCTG TCAAGTATGTGGAGTGTTCTGCACTTACACA	SEQ ID NO: 2396

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
CDC42BPA	NM_003607.2	GAGCTGAAAGACGCACACTGTCAGAGGAAACTGGCCATGCAGGAATTCATGGAGATCAATGAGCGGC	SEQ ID NO: 2397
CDC6	NM_001254.2	GCAACACTCCCCATTTACCTCCTTGTTCTCCACCAAAGCAAGGCAAGAAAGAGAATGGTCCCCCTCA	SEQ ID NO: 2398
CDCA7 v2	NM_145810.1	AAGACCGTGGATGGCTACATGAATGAAGATGACCTGCCCAGAAGCCGTCGCTCCAGATCATCCGTGACCCT	SEQ ID NO: 2399
CDH1	NM_004360.2	TGAGTGTCCCCCGGTATCTTCCCCGCCCTGCCAATCCCGATGAAATTGGAAATTTTATTGATGAAAATCTGAAAGCGGCTG	SEQ ID NO: 2400
CDH11	NM_001797.2	GTCGGCAGAAGCAGGACTTGTACCTTCTGCCCATAGTGATCAGCGATGGCGGCATCCCGCCCATGAGTAG	SEQ ID NO: 2401
CDH3	NM_001793.3	ACCCATGTACCGTCCTCGGCCAGCCAACCCAGATGAAATCGGCAACTTTATAATTGAGAACCTGAAGGCGG	SEQ ID NO: 2402
CDK2	NM_001798.2	AATGCTGCACTACGACCCTAACAAGCGGATTTCGGCCAAGGCAGCCCTGGCTCACCCTTTCTTCCAGGATGTGACCAA	SEQ ID NO: 2403
CDX1	NM_001804.1	AGCAACACCAGCCTCCTGGCCACCTCCTCTCCAATGCCTGTGAAAGAGGAGTTTCTGCCATAGCCC	SEQ ID NO: 2404
Cdx2	NM_001265.2	GGGCAGGCAAGGTTTACACTGCGGAAGCCAAAGGCAGCTAAGATAGAAAGCTGGACTGACCAAAGAC	SEQ ID NO: 2405
CEACAM1	NM_001712.2	ACTTGCCTGTTCAGAGCACTCATTCCTTCCCACCCCCAGTCCTGTCCTATCACTCTAATTCGGATTTGCCA	SEQ ID NO: 2406
CEACAM6	NM_002483.2	CACAGCCTCACTTCTAACCTTCTGGAACCCACCCACCACTGCCAAGCTCACTATTGAATCCACGCCATTCAA	SEQ ID NO: 2407
CEBPB	NM_005194.2	GCAACCCACGTGTAACTGTCAGCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCTACGGGCTTGT	SEQ ID NO: 2408
CEGP1	NM_020974.1	TGACAATCAGCACACCTGCATTCACCGCTCGGAAGAGGGCCTGAGCTGCATGAATAAGGATCACGGCTGTAGTCACA	SEQ ID NO: 2409
CENPA	NM_001809.2	TAAATTCACTCGTGGTGTGGACTTCAATTGGCAAGCCCAGGCCCTATTGGCCCTACAAGAGGC	SEQ ID NO: 2410
CENPE	NM_001813.1	GGATGCTGGTGACCTCTTCTTCCCTCACGTTGCAACAGGAATTAAAGGCTAAAAGAAAACGAAGAGTTACTTGGTGCCTTGGC	SEQ ID NO: 2411
CENPF	NM_016343.2	CTCCCGTCAACAGCGTTCTTTCCAAACACTGGACCAGGAGTGCATCCAGATGAAGGCCAGACTCACCC	SEQ ID NO: 2412
CES2	NM_003869.4	ACTTTGCGAGAAATGGGAACCCCAATGGCGAGGGTCTGCCACACTGGCCGCTGTTCGACCAGGAGGAGCAATACCTG	SEQ ID NO: 2413
CGA (CHGA official)	NM_001275.2	CTGAAGGAGCTCCAAGACCTCGCTCTCCAAGGCGCCAAGGAGAGGGCACATCAGCAGAAGAAACACAGCGGTTTTG	SEQ ID NO: 2414
CGB	NM_000737.2	CCACCATAGGCAGAGGCAGGCCTTCCTACACCCTACTCCCTGTGCCTCCAGCCTCGACTAGTCCCTAGCACTCGACGACT	SEQ ID NO: 2415
CHAF1B	NM_005441.1	GAGGCCAGTGGTGGAAACAGGTGTGGAGCTGATGAGTCTGCCCTACCGCCTGGTGTTTGCTGTGGCCTCGGA	SEQ ID NO: 2416
CHD2	NM_001271.1	CTCTGTGCGAGGCTGTCAGCCACACTAGGTATCAGGGATCCCGAGATGGGTACCAGCCCACAGTCCTTACC	SEQ ID NO: 2417
CHFR	NM_018223.1	AAGGAAGTGGTCCCTCTGTGGCAAGTGATGAAGTCTCCAGCTTTGCCTCAGCTCTCCCAGACAGAAAGACTGCGTC	SEQ ID NO: 2418
Chk1	NM_001274.1	GATAAATTGGTACAAGGGATCAGCTTTTCCCAGCCCACATGTCCTGATCATATGCTTTTGAATAGTCAGTTACTTGGCACCC	SEQ ID NO: 2419
Chk2	NM_007194.1	ATGTGGAACCCCCACCTACTTGGCGCCTGAAGTTCTTGTTTCTGTTGGGACTGCTGGGTATAACCGTGCTGTGGACTG	SEQ ID NO: 2420
CIAP1	NM_001166.2	TGCCTGTGGTGGGAAGCTCAGTAACTGGGAACCAAAGGATGATGCTATGTCAGAACACCGGAGGCATTTTCC	SEQ ID NO: 2421

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
cIAP2	NM_001165.2	GGATATTTCCGTGGCTCTTATTCAAACTCTCCATCAAATCCTGTAAACTCCAGAGCAAATCAAGATTTTTCTGCCTTGATGAGAAG	SEQ ID NO: 2422
CKS1B	NM_001826.1	GGTCCCTAAAACCCATCTGATGTCTGAATCTGAATGGAGGAATCTTGGCGTTCAGCAGAGTCAGGGATGGGTCCATTA	SEQ ID NO: 2423
CKS2	NM_001827.1	GGCTGGACGTGGTTTTGTCTGCTGCGCCCGCTCTTCGCGCTCTCGTTTCATTTTCTGCAGCG	SEQ ID NO: 2424
Claudin 4	NM_001305.2	GGCTGCTTTGCTGCAACTGTCCACCCCGCACAGACAAGCCTTACTCCGCCAAGTATTCTGCTGCCCGCTCTG	SEQ ID NO: 2425
CLDN1	NM_021101.3	TCTGGGAGGTGCCCTACTTTGCTGTTCCTGTCCCCGAAAAACAACCTCTTACCCAACACCAAGGCCCTATCCA	SEQ ID NO: 2426
CLDN7	NM_001307.3	GGTCTGCCCTAGTCATCCTGGGAGGTGCACTGCTCTCCTGTTCCTGTCCTGGGAATGAGAGCAAGGCTGGGTAC	SEQ ID NO: 2427
CLIC1	NM_001288.3	CGGTACTTGAGCAATGCCTACGCCCGGGAAGAATTCGCTTCCACCTGTCCAGATGATGAGGAGATCGA	SEQ ID NO: 2428
CLTC	NM_004859.1	ACCGTATGGACAGCCACAGCCTGGCTTTGGGTACAGCATGTGAGATGAAGCGCTGATCCTGTAGTCA	SEQ ID NO: 2429
CLU	NM_001831.1	CCCCAGGATACCTACCACTACCTGCCCTTCAGCCTGCCCCACCGGAGGCCTCACTTCTTCTTTCCCAAGTCCCGCA	SEQ ID NO: 2430
cMet	NM_000245.1	GACATTTCCAGTCCTGCAGTCAATGCCTCTCTGCCCCACCCTTTGTTCAGTGTGGCTGGTGCCACGACAAATGTGTGCGATCGGAG	SEQ ID NO: 2431
cMYC	NM_002467.1	TCCCTCCACTCGGAAGGACTATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGTCCTGAGACAGATCAGCAACAACCG	SEQ ID NO: 2432
CNN	NM_001299.2	TCCACCCTCCTGGCTTTGGCCAGCATGGCGAAGACGAAAGGAAACAAGGTGAACGTGGGAGTGA	SEQ ID NO: 2433
COL1A1	NM_000088.2	GTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTG	SEQ ID NO: 2434
COL1A2	NM_000089.2	CAGCCAAGAACTGGTATAGGAGCTCCAAGGACAAGAAACACGTCTGGCTAGGAGAAACTATCAATGCTGGCAGCCAGTTT	SEQ ID NO: 2435
COPS3	NM_003653.2	ATGCCCAGTGTTCCTGACTTCGAAACGCTATTCTCACAGGTTCAGCTCTTCATCAGCACTTGTAATGGGGAG	SEQ ID NO: 2436
COX2	NM_000963.1	TCTGCAGAGTTGGAAGCACTCTATGGTGACATCGATGCTGTGGAGCTGTATCCTGCCCTTCTGGTAGAAAAGCCTCGGC	SEQ ID NO: 2437
COX3	MITO_COX3	TCGAGTCTCCCTTCACCATTTCCGACGGCATCTACGGCTCAACATTTTTTGTAGCCACAGGCTTCCACGGACTTCACGTC	SEQ ID NO: 2438
CP	NM_000096.1	CGTGAGTACACAGATGCCTCCTTCACAAATCGAAAGGAGAGAGGCCCTGAAGAAGAGCATCTTGGCATCCTGG	SEQ ID NO: 2439
CRBP	NM_002899.2	TGGTCTGCAAGCAAGTATTCAAGAAGGTGCAGTGAGGCCCAAGCAGACAACCTTGTCCCAACCAATCAGC	SEQ ID NO: 2440
CREBBP	NM_004380.1	TGGGAAGCAGCTGTGTACCATTCCTCGCGATGCTGCCTACTACAGCTATCAGAATAGGTATCATTTCTGTGAGAAGTGTTTC	SEQ ID NO: 2441
CRIP2	NM_001312.1	GTGCTACGCCACCCTGTTCGGACCCAAAGGCGTGAACATCGGGGGCGCGGGCTCCTACATCTACGAGAAGCCCCTG	SEQ ID NO: 2442
cripto (TDGF1 official)	NM_003212.1	GGGTCTGTGCCCCATGACACCTGGCTGCCCAAGAAGTGTTCCCTGTGTAAATGCTGGCACGGTCA	SEQ ID NO: 2443
CRK(a)	NM_016823.2	CTCCCTAACCTCCAGAATGGGCCCATATATGCCAGGGTTATCCAGAAGCGAGTCCCCAATGCCTACGACAAGACA	SEQ ID NO: 2444
CRMP1	NM_001313.1	AAGGTTTTTGGATTGCAAGGGGTTTCCAGGGGCATGTATGACGGTCCTGTGTACGAGGTACCAGCTACACCC	SEQ ID NO: 2445
CRYAB	NM_001885.1	GATGTGATTGAGGTGCATGGAAAACATGAAGAGCGCCAGGATGAACATGGTTTCATCTCCAGGGAGTTC	SEQ ID NO: 2446

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
CSEL1	NM_001316.2	TTACGCAGCTCATGCTCTTGAACGGCTCTTTACTATGCGAGGGCCTAACAATGCCACTCTCTTTACAGCTGC	SEQ ID NO: 2447
CSF1	NM_000757.3	TGCAGCGGCTGATTGACAGTCAGATGGAGACCTCGTGCCAAATTACATTTGAGTTTGTAGACCAGGAACAGTTG	SEQ ID NO: 2448
CSK (SRC)	NM_004383.1	CCTGAACATGAAGGAGCTGAAGCTGCTGCAGACCATCGGGAAGGGGGAGTTCGGAGACGTGATG	SEQ ID NO: 2449
CTAG1B	NM_001327.1	GCTCTCCATCAGCTCCTGTCTCCAGCAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTT	SEQ ID NO: 2450
CTGF	NM_001901.1	GAGTTCAAGTGCCCTGACGGCGAGGTCATGAAGAAGAACATGATGTTCATCAAGACCTGTGCCTGCCATTACAACT	SEQ ID NO: 2451
CTHRC1	NM_138455.2	GCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGA	SEQ ID NO: 2452
CTLA4	NM_005214.2	CACTGAGGTCCGGGTGACAGTGCTTCGGCAGGCTGACAGCCAGGTGACTGAAGTCTGTGCGGCAACCTAC	SEQ ID NO: 2453
CTNNBIP1	NM_020248.2	GTTTTCCAGGTCGGAGACGGAAGACCGGAGGCAGTAGCTGCAAAGCCCTTGGAACACCCTGGATGCT	SEQ ID NO: 2454
CTSB	NM_001908.1	GGCCGAGATCTACAAAAACGGCCCCGTGGAGGGAGCTTTCTCTGTGTATTCGGACTTCCTGC	SEQ ID NO: 2455
CTSD	NM_001909.1	GTACATGATCCCCTGTGAGAAGGTGTCCACCCTGCCCGCGATCACACTGAAGCTGGGAGGCAAAGGCTACAAGCTGTCCC	SEQ ID NO: 2456
CTSH	NM_004390.1	GCAAGTTCCAACCTGGAAAGGCCATCGGCTTTGTCAAGGATGTAGCCAACATCACAATCTATGACGAGGAAGCGATG	SEQ ID NO: 2457
CTSL	NM_001912.1	GGGAGGCTTATCTCACTGAGTGAGCAGAATCTGGTAGACTGCTCTGGGCCTCAAGGCAATGAAGGCTGCAATGG	SEQ ID NO: 2458
CTSL2	NM_001333.2	TGTCTCACTGAGCGAGCAGAATCTGGTGGACTGTTCGCGTCCTCAAGGCAATCAGGGCTGCAATGGT	SEQ ID NO: 2459
CUL1	NM_003592.2	ATGCCCTGGTAATGTCTGCATTCAACAATGACGCTGGCTTTGTGGCTGCTCTTGATAAGGCTTGTGGTCGC	SEQ ID NO: 2460
CUL4A	NM_003589.1	AAGCATCTTCCTGTTCTTGGACCGCACCTATGTGCTGCAGAACTCCACGCTGCCCTCCATCTGGGATATGGGATT	SEQ ID NO: 2461
CXCL12	NM_000609.3	GAGCTACAGATGCCCATGCCGATTCTTCGAAAGCCATGTTGCCAGAGCCAACGTCAAGCATCTCAAA	SEQ ID NO: 2462
CXCR4	NM_003467.1	TGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTGTTCCAGTTTCAGCACATCATGGTTGGCCTTATCCT	SEQ ID NO: 2463
CYBA	NM_000101.1	GGTGCCTACTCCATTGTGGCGGGCGTGTTTGTGTGCCTGCTGGAGTACCCCCGGGGGAAGAGGAAGAAGGGCTCCAC	SEQ ID NO: 2464
CYP1B1	NM_000104.2	CCAGCTTTGTGCCTGTCACTATTCCTCATGCCACCACTGCCAACACCTCTGTCTTGGGCTACCACATTCCC	SEQ ID NO: 2465
CYP2C8	NM_000770.2	CCGTGTTCAAGAGGAAGCTCACTGCCTTGTGGAGGAGTTGAGAAAAACCAAGGCTTCACCCTGTGATCCCACT	SEQ ID NO: 2466
CYP3A4	NM_017460.3	AGAACAAGGACAACATAGATCCTTACATATACACACCCTTTGGAAGTGGACCCAGAAACTGCATTGGCATGAGGTTTGC	SEQ ID NO: 2467
CYR61	NM_001554.3	TGCTCATTCTTGAGGAGCATTAAGGTATTTCGAAACTGCCAAGGGTGCTGGTGCGGATGGACACTAATGCAGCCAC	SEQ ID NO: 2468
DAPK1	NM_004938.1	CGCTGACATCATGAATGTTCCTCGACCGGCTGGAGGCGAGTTTGGATATGACAAAGACACATCGTTGCTGAAAGAGA	SEQ ID NO: 2469
DCC	NM_005215.1	AAATGTCCTCCTCGACTGCTCCGCGGAGTCCGACCGAGGAGTTCCAGTGATCAAGTGGAAGAAAGATGGCATTCA	SEQ ID NO: 2470
DCC_exons18-23	X76132_18-23	GGTCACCGTTGGTGTCATCACAGTGCTGGTAGTGGTCATCGTGGCTGTGATTTGCACCCGACGCTC	SEQ ID NO: 2471

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
DCC_exons6-7	X76132_6-7	ATGGAGATGTGGTCATTCCTAG TGATTATTTTCAGATAGTGGGAGGAAGCAACTTACGGATACTTGGGGTGGTG	SEQ ID NO: 2472
DCK	NM_000788.1	GCCGCCACAAGACTAAGGAATGGCCACCCCGCCCAAGAGA AGCTGCCCGTCTTTCTCAGCCAGCTCTGAGGGGACCCG CATCAAGAAAATCTCCATCGAAGGGAACATCG	SEQ ID NO: 2473
DDB1	NM_001923.2	TGCGGATCATCCGGAATGGAATTGGAATCCACGAGCA TGCCAGCATTGACTTACCAGGCATCAAAGGA	SEQ ID NO: 2474
DET1	NM_017996.2	CTTGTGGAGATCACCCAATCAGGTTCTATGCCCGGGACTCGG GCCTGCTCAAGTTTGAGATCCAGGCGGG	SEQ ID NO: 2475
DHFR	NM_000791.2	TTGCTATAACTAAGTGCTTCTCCAAGACCCCAACTGAGTCC CCAGCACCTGCTACAGTGAGCTGCCATTCCAC	SEQ ID NO: 2476
DHPS	NM_013407.1	GGGAGAACGGGATCAATAGGATCGGAAACCTGCTGGTGCCC AATGAGAATTACTGCAAGTTTGAGGACTGGCTGATGC	SEQ ID NO: 2477
DIABLO	NM_019887.1	CACAATGGCGGCTCTGAAGAGTTGGCTGTCGCGCAG CGTAACTTCATTCTTCAGGTACAGACAGTGTTTGTGT	SEQ ID NO: 2478
DIAPH1	NM_005219.2	CAAGCAGTCAAGGAGAACCAGAAGCGGCGGGAGACA GAAGAAAAGATGAGGCGAGCAAAACT	SEQ ID NO: 2479
DICER1	NM_177438.1	TCCAATTCCAGCATCACTGTGGAGAAAAGCTG TTTGTCTCCCCAGCATACTTTATCGCCTTCACTGCC	SEQ ID NO: 2480
DKK1	NM_012242.1	TGACAACTACCAGCCGTACCCGTGCGCAGAGGACGAGGA GTGCGGCACTGATGAGTACTGCGCTAGTCCC	SEQ ID NO: 2481
DLC1	NM_006094.3	GATTCAGACGAGGATGAGCCTTGTGCCATCAGTGGCAAATGG ACTTTCCAAAGGGACAGCAAGAGGTG	SEQ ID NO: 2482
DPYD	NM_000110.2	AGGACGCAAGGAGGGTTTGTCACTGGCAGACTCGAGACTGTAGGC ACTGCCATGGCCCCTGTGCTCAGTAAGGACTCGGCGGACATC	SEQ ID NO: 2483
DR4	NM_003844.1	TGCACAGAGGGTGTGGGTTACACCAATGCTTCCAACAATTTGTTT GCTTGCCTCCCATGTACAGCTTGTAAATCAGATGAAGA	SEQ ID NO: 2484
DR5	NM_003842.2	CTCTGAGACAGTGCTTCGATGACTTTGCAGACTTGGTGCCCTTTGA CTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGG	SEQ ID NO: 2485
DRG1	NM_004147.3	CCTGGATCTCCCAGGTATCATTGAAGGTGCCAAGGATGGG AAAGGTAGAGGTCGTCAAGTCATTGCA	SEQ ID NO: 2486
DSP	NM_004415.1	TGGCACTACTGCATGATTGACATAGAGAAGATCAGGGCCATGAC AATCGCCAAGCTGAAAACAATGCGGCAGG	SEQ ID NO: 2487
DTYMK	NM_012145.1	AAATCGCTGGGAACAAGTGCCGTTAATTAAGGAAAAGTTGAGC CAGGGCGTGACCCTCGTCGTGGACAGATACGCATT	SEQ ID NO: 2488
DUSP1	NM_004417.2	AGACATCAGCTCCTGGTTCAACGAGGCCATTGACTTCATAGACTCC ATCAAGAATGCTGGAGGAAGGGTGTTTGTC	SEQ ID NO: 2489
DUSP2	NM_004418.2	TATCCCTGTGGAGGACAACCAGATGGTGGAGATCAGTGCCT GGTTCCAGGAGGCCATAGGCTTCATTGACTGGGTG	SEQ ID NO: 2490
DUT	NM_001948.2	ACACATGGAGTGCTTCTGGAACTATCAGCCCACTTGACCAC CCAGTTTGTGGAAGCACAGGCAAGAG	SEQ ID NO: 2491
DYRK1B	NM_004714.1	AGCATGACACGGAGATGAAGTACTATATAGTACAC CTGAAGCGGCACTTCATGTTCCGGAACCACCTGTGCCTGGTATT	SEQ ID NO: 2492
E2F1	NM_005225.1	ACTCCCTCTACCCTTGAGCAAGGGCAGGGGTCCCTGAG CTGTTCTTCTGCCCCATACTGAAGGAACTGAGGCCTG	SEQ ID NO: 2493
EDN1 endothelin	NM_001955.1	TGCCACCTGGACATCATTTGGGTCAACACTCCCGAGCACGT TGTTCCGTATGGACTTGGAAGCCCTAGGTCCA	SEQ ID NO: 2494
EFNA1	NM_004428.2	TACATCTCCAAACCCATCCACCAGCATGAAGACCGCTGCT TGAGGTTGAAGGTGACTGTCAGTGGCAA	SEQ ID NO: 2495
EFNA3	NM_004952.3	ACTACATCTCCACGCCCACTCACAACCTGCACTGGAAGTGTC TGAGGATGAAGGTGTTCGTCTGCTG	SEQ ID NO: 2496

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
EFNB1	NM_004429.3	GGAGCCCGTATCCTGGAGCTCCCTCAACCCCAAGTTCCTGAGTGGGAAGGGCTTGGTGATCTATCC	SEQ ID NO: 2497
EFNB2	NM_004093.2	TGACATTATCATCCCGCTAAGGACTGCGGACAGCGTCTTCTGCCCTCACTACGAGAAGGTCAGCGGGGACTAC	SEQ ID NO: 2498
EFP	NM_005082.2	TTGAACAGAGCCTGACCAAGAGGGATGAGTTCGAGTTTCTGGAGAAAGCATCAAAACTGCGAGGAATCTCAACA	SEQ ID NO: 2499
EGFR	NM_005228.1	TGTCGATGGACTTCCAGAACCACCTGGGCAGCTGCCAAAAGTGTGATCCAAGCTGTCCCAAT	SEQ ID NO: 2500
EGLN1	NM_022051.1	TCAATGGCCGGACGAAAGCCATGGTTGCTTGTTATCCGGGCAATGGAACGGGTTATGTACGTCATGTTGATAATCCAAA	SEQ ID NO: 2501
EGLN3	NM_022073.2	GCTGGTCCTCTACTGCGGGAGCCGGCTGGGCAAATACTACGTCAAGGAGAGGTCTAAGGCAATGGTGG	SEQ ID NO: 2502
EGR1	NM_001964.2	GTCCCCGCTGCAGATCTCTGACCCGTTCGGATCCTTTCCTCACTCGCCCACCATGGACAACTACCCTAAGCTGGAG	SEQ ID NO: 2503
EGR3	NM_004430.2	CCATGTGGATGAATGAGGTGTCTCCTTTCCATACCCAGTCTCACCTTCTCCCCACCCTACCTCACCTCTTCTCAGGCA	SEQ ID NO: 2504
EI24	NM_004879.2	AAAGTGGTGAATGCCATTTGGTTTCAGGATATAGCTGACCTGGCATTTGAGGTATCAGGGAGGAAGCCTCAC	SEQ ID NO: 2505
EIF4E	NM_001968.1	GATCTAAGATGGCGACTGTCGAACCGGAAACCACCCCTACTCCTAATCCCCCGACTACAGAAGAGGAGAAAACGGAATCTAA	SEQ ID NO: 2506
EIF4EL3	NM_004846.1	AAGCCGCGGTTGAATGTGCCATGACCCTCTCCCTCTCTGGATGGCACCATCATTGAAGCTGGCGTCA	SEQ ID NO: 2507
ELAVL1	NM_001419.2	GACAGGAGGCCTCTATCCTGTCCCTCCACCCCACCCTCCACCTCAATCCCCTCCCATCTTCCCCAGACCTACCTCAC	SEQ ID NO: 2508
EMP1	NM_001423.1	GCTAGTACTTTGATGCTCCCTTGATGGGGTCCAGAGAGCCTCCCTGCAGCCACCAGACTTGGCCTCCAGCTGTTC	SEQ ID NO: 2509
EMR3	NM_032571.2	TGGCCTACCTCTTCACCATCATCAACAGCCTCCAAGGCTTCTTCATCTTCTTGGTCTACTGCCTCCTCA	SEQ ID NO: 2510
EMS1	NM_005231.2	GGCAGTGTCACTGAGTCCTTGAAATCCTCCCCTGCCCCGCGGGTCTCTGGATTGGGACGCACAGTGCA	SEQ ID NO: 2511
ENO1	NM_001428.2	CAAGGCCGTGAACGAGAAGTCCTGCAACTGCCTCCTGCTCAAAGTCAACCAGATTGGCTCCGTGACCG	SEQ ID NO: 2512
EP300	NM_001429.1	AGCCCCAGCAACTACAGTCTGGGATGCCAAGGCCAGCCATGATGTCAGTGGCCCAGCATGGTCAACCTTTGAACA	SEQ ID NO: 2513
EPAS1	NM_001430.3	AAGCCTTGGAGGGTTTCATTGCCGTGGTGACCCAAGATGGCGACATGATCTTTCTGTCAGAAAACATCAGCA	SEQ ID NO: 2514
EpCAM	NM_002354.1	GGGCCCTCCAGAACAATGATGGGCTTTATGATCCTGACTGCGATGAGAGCGGGCTCTTTAAGGCCAAGCAGTGCA	SEQ ID NO: 2515
EPHA2	NM_004431.2	CGCCTGTTCACCAAGATTGACACCATTGCGCCCGATGAGATCACCGTCAGCAGCGACTTCGAGGCACGCCAC	SEQ ID NO: 2516
EPHB2	NM_004442.4	CAACCAGGCAGCTCCATCGGCAGTGTCCATCATGCATCAGGTGAGCCGCACCGTGGACAGCATTAC	SEQ ID NO: 2517
EPHB4	NM_004444.3	TGAACGGGGTATCCTCCTTAGCCACGGGGCCCGTCCCATTTGAGCCTGTCAATGTCACCACTGACCGAGAGGTACCT	SEQ ID NO: 2518
EphB6	NM_004445.1	ACTGGTCCTCCATCGGCTCCCCAGGAGCTTTGGTTTGAGGTGCAAGGCTCAGCACTCATGCTACACTGG	SEQ ID NO: 2519
EPM2A	NM_005670.2	ACTGTGGCACTTAGGGGAGATGACATTTGCTTTGGGCAGAGGCAGCTAGCCAGGACACATTTCCACT	SEQ ID NO: 2520
ErbB3	NM_001982.1	CGGTTATGTCATGCCAGATACACACCTCAAAGGTACTCCCTCCTCCCGGGAAGGCACCCTTTCTTCAGTGGGTCTCAGTTC	SEQ ID NO: 2521

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
ERCC1	NM_001983.1	GTCCAGGTGGATGTGAAAGATCCCCAGCAGGCCCTCAGAGGAGCTGGCTAAGATGTGTATCCTGGCCG	SEQ ID NO: 2522
ERCC2	NM_000400.2	TGGCCTTCTTCACCAGCTACCAGTACATGGAGAGCACCGTGGCCTCCTGGTATGAGCAGGGGATCCTTG	SEQ ID NO: 2523
EREG	NM_001432.1	ATAACAAAGTGTAGCTCTGACATGAATGGCTATTGTTTGCATGGACAGTGCATCTATCTGGTGGACATGAGTCAAAACTACTGCAGGTGTG	SEQ ID NO: 2524
ERK1	Z11696.1	ACGGATCACAGTGGAGGAAGCGCTGGCTCACCCCTACCTGGAGCAGTACTATGACCCGACGGATGAG	SEQ ID NO: 2525
ERK2	NM_002745.1	AGTTCTTGACCCCTGGTCCTGTCTCCAGCCCGTCTTGGCTTATCCACTTTGACTCCTTTGAGCCGTTT	SEQ ID NO: 2526
ESPL1	NM_012291.1	ACCCCCAGACCGGATCAGGCAAGCTGGCCCTCATGTCCCCTTCACGGTGTTTGAGGAAGTCTGCCCTACA	SEQ ID NO: 2527
EstR1	NM_000125.1	CGTGGTGCCCCTCTATGACCTGCTGCTGGAGATGCTGGACGCCCACCGCCTACATGCGCCCACTAGCC	SEQ ID NO: 2528
ETV4	NM_001986.1	TCCAGTGCCTATGACCCCCCCAGACAAATCGCCATCAAGTCCCCTGCCCCTGGTGCCCTTGGACAGT	SEQ ID NO: 2529
F3	NM_001993.2	GTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGAGCACCGGTT	SEQ ID NO: 2530
FABP4	NM_001442.1	GCTTTGCCACCAGGAAAGTGGCTGGCATGGCCAAACCTAACATGATCATCAGTGTGAATGGGGATG	SEQ ID NO: 2531
FAP	NM_004460.2	CTGACCAGAACCACGGCTTATCCGGCCTGTCCACGAACCACTTATACACCCACATGACCCACTTCC	SEQ ID NO: 2532
fas	NM_000043.1	GGATTGCTCAACAACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTTACGTCTGTTGCTAGATTATCGTCCAAAAGTGTTAATGCC	SEQ ID NO: 2533
fasI	NM_000639.1	GCACTTTGGGATTCTTTCCATTATGATTCTTTGTTACAGGCACCGAGAATGTTGTATTCAGTGAGGGTCTTCTTACATGC	SEQ ID NO: 2534
FASN	NM_004104.4	GCCTCTTCCTGTTCGACGGCTCGCCCACCTACGTACTGGCCTACACCCAGAGCTACCGGGCAAAGC	SEQ ID NO: 2535
FBXO5	NM_012177.2	GGCTATTCCTCATTTTCTCTACAAAGTGGCCTCAGTGAACATGAAGAAGGTAGCCTCCTGGAGGAGAATTTCGGTGACAGTCTACAATCC	SEQ ID NO: 2536
FBXW7	NM_033632.1	CCCCAGTTTCAACGAGACTTCATTTCATTGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAAC	SEQ ID NO: 2537
FDXR	NM_004110.2	GAGATGATTCAGTTACCGGGAGCCCGGCCCATTTTGGATCCTGTGGATTTCTTGGGTCTCCAGGACAAGAT	SEQ ID NO: 2538
FES	NM_002005.2	CTCTGCAGGCCTAGGTGCAGCTCCTCAGCGGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCCTGG	SEQ ID NO: 2539
FGF18	NM_003862.1	CGGTAGTCAAGTCCGGATCAAGGGCAAGGAGACGGAATTCTACCTGTGCATGAACCGCAAAGGCAAGC	SEQ ID NO: 2540
FGF2	NM_002006.2	AGATGCAGGAGAGAGGAAGCCTTGCAAACCTGCAGACTGCTTTTTGCCCAATATAGATTGGGTAAGGCTGCAAAAC	SEQ ID NO: 2541
FGFR1	NM_023109.1	CACGGGACATTCACCACATCGACTACTATAAAAAGACAACCAACGGCCGACTGCCTGTGAAGTGGATGGCACCC	SEQ ID NO: 2542
FGFR2 isoform 1	NM_000141.2	GAGGGACTGTTGGCATGCAGTGCCCTCCCAGAGACCAACGTTCAAGCAGTTGGTAGAAGACTTGGATCGAATTCTCACTC	SEQ ID NO: 2543
FHIT	NM_002012.1	CCAGTGGAGCGCTTCCATGACCTGCGTCCTGATGAAGTGGCCGATTTGTTTCAGACGACCCAGAGAG	SEQ ID NO: 2544
FIGF	NM_004469.2	GGTTCCAGCTTTCTGTAGCTGTAAGCATTGGTGGCCACACCACCTCCTTACAAAGCAACTAGAACCTGCGGC	SEQ ID NO: 2545
FLJ12455	NM_022078.1	CCACCAGCATGAAGTTTCGGACAGACATGGCCTTTGTGAGGGGTTCCAGTTGTGCTTCAGACAGCC	SEQ ID NO: 2546

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
FLJ20712	AK000719.1	GCCACACAAACATGCTCCTGCTCCTGGCGGAGGCAGAGC TGCTGGGAAAGACATTTCGGAAGTTTCCTGTGGC	SEQ ID NO: 2547
FLT1	NM_002019.1	GGCTCCCGAATCTATCTTTGACAAAATCTACAGCACCAAGA GCGACGTGTGGTCTTACGGAGTATTGCTGTGGGA	SEQ ID NO: 2548
FLT4	NM_002020.1	ACCAAGAAGCTGAGGACCTGTGGCTGAGCCCGCTGACCATG GAAGATCTTGTCTGCTACAGCTTCCAGG	SEQ ID NO: 2549
FOS	NM_005252.2	CGAGCCCTTTGATGACTTCCTGTTCCCAGCATC ATCCAGGCCCAGTGGCTCTGAGACAGCCCGCTCC	SEQ ID NO: 2550
FOXO3A	NM_001455.1	TGAAGTCCAGGACGATGATGCGCCTCTCTCGCCCATGCTCTACAGC AGCTCAGCCAGCCTGTCACCTTCAGTAAGCAAGCCGT	SEQ ID NO: 2551
FPGS	NM_004957.3	CAGCCCTGCCAGTTTGACTATGCCGTCTTCTGCCCTA ACCTGACAGAGGTGTCATCCACAGGCAAC	SEQ ID NO: 2552
FRP1	NM_003012.2	TTGGTACCTGTGGGTTAGCATCAAGTTCTCCCCAGGGTAGA ATTCAATCAGAGCTCCAGTTTGCATTTGGATGTG	SEQ ID NO: 2553
FST	NM_006350.2	GTAAGTCGGATGAGCCTGTCTGTGCCAGTGACAATGCCACT TATGCCAGCGAGTGTGCCATGAAGGAAGCTG	SEQ ID NO: 2554
Furin	NM_002569.1	AAGTCCTCGATACGCACTATAGCACCGAGAATGACGTGGAGACCAT CCGGGCCAGCGTCTGCGCCCCCTGCCACGCCTCATGTGCCACATGCCAG	SEQ ID NO: 2555
FUS	NM_004960.1	GGATAATTCAGACAACAACACCATCTTTGTGCAA GGCCTGGGTGAGAATGTTACAATTGAGTCTGTGGCTGATTACTTCA	SEQ ID NO: 2556
FUT1	NM_000148.1	CCGTGCTCATTGCTAACCACTGTCTGTCCCT GAACTCCCAGAACCACTACATCTGGCTTTGGGCAG	SEQ ID NO: 2557
FUT3	NM_000149.1	CAGTTCGGTCCAACAGAGAAAGCAGGCAACCA CCATGTCATTTGAAAACAGTTTCATCGGGATATAATTCGCA	SEQ ID NO: 2558
FUT6	NM_000150.1	CGTGTGTCTCAAGACGATCCCACTGTGTACCCTAAT GGGTCCCGCTTCCCAGACAGCACAGGGACC	SEQ ID NO: 2559
FXYD5	NM_014164.4	AGAGCACCAAAGCAGCTCATCCCACTGATGACAC CACGACGCTCTCTGAGAGACCATCCCCAAGCAC	SEQ ID NO: 2560
FYN	NM_002037.3	GAAGCGCAGATCATGAAGAAGCTGAAGCACGACAAG CTGGTCCAGCTCTATGCAGTGGTGTCTGAGGAG	SEQ ID NO: 2561
FZD1	NM_003505.1	GGTGCACCAGTTCTACCCTCTAGTGAAAGTGCAGTGTTCC GCTGAGCTCAAGTTCTTCCTGTGCTCCATGTACGC	SEQ ID NO: 2562
FZD2	NM_001466.2	TGGATCCTCACCTGGTCGGTGCTGTGCTGCGCTTCCACCTTCTT CACTGTCACCACGTACTTGGTAGACATGCAGCGC	SEQ ID NO: 2563
FZD6	NM_003506.2	AATGAGAGAGGTGAAAGCGGACGGAGCTAGCACC CCCAGGTTAAGAGAACAGGACTGTGGTGAACCT	SEQ ID NO: 2564
G-Catenin	NM_002230.1	TCAGCAGCAAGGGCATCATGGAGGAGGATGAG GCCTGCGGGCGCCAGTACACGCTCAAGAAAACCACC	SEQ ID NO: 2565
G1P2	NM_005101.1	CAACGAATTCCAGGTGTCCCTGAGCAGCTCCATGTC GGTGTCAGAGCTGAAGGCGCAGATC	SEQ ID NO: 2566
GADD45	NM_001924.2	GTGCTGGTGACGAATCCACATTCATCTCAATGGAAGGATCC TGCCTTAAGTCAACTTATTTGTTTTTGCCGGG	SEQ ID NO: 2567
GADD45B	NM_015675.1	ACCCTCGACAAGACCACACTTTGGGACTTGGGAGCTG GGGCTGAAGTTGCTCTGTACCCATGAACTCCCA	SEQ ID NO: 2568
GADD45G	NM_006705.2	CGCGCTGCAGATCCATTTTACGCTGATCCAGGCTTTC TGCTGCGAGAACGACATCGACATAGTGCG	SEQ ID NO: 2569
GAGE4	NM_001474.1	GGAACAGGGTCACCCACAGACTGGGTGTGAGTGTGAAGA TGGTCCTGATGGGCAGGAGATGGACCCGCCAAATC	SEQ ID NO: 2570
GBP1	NM_002053.1	TTGGGAAATATTTGGGCATTGGTCTGGCCAAGTCTACAAT GTCCCAATATCAAGGACAACCACCCTAGCTTCT	SEQ ID NO: 2571

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
GBP2	NM_004120.2	GCATGGGAACCATCAACCAGCAGGCCATGGACCAACTTCACTA TGTGACAGAGCTGACAGATCGAATCAAGGCAAACTCCTCA	SEQ ID NO: 2572
GCLC	NM_001498.1	CTGTTGCAGGAAGGCATTGATCATCTCCTGGCCC AGCATGTTGCTCATCTCTTTATTAGAGACCCACTGAC	SEQ ID NO: 2573
GCLM	NM_002061.1	TGTAGAATCAAACTCTTCATCATCAACTAGAAGTGCAGTTGACA TGGCCTGTTCAGTCCTTGGAGTTGCACAGCTGGATTCTGTG	SEQ ID NO: 2574
GCNT1	NM_001490.3	TGGTGCTTGGAGCATAGAAGACTGCCCTTCACAAAG GAAATCCCTGATTATTGTTTGAAATGCTGAGGACGTTGC	SEQ ID NO: 2575
GDF15	NM_004864.1	CGCTCCAGACCTATGATGACTTGTTAGCCAA AGACTGCCACTGCATATGAGCAGTCCTGGTCCTTCCACTGT	SEQ ID NO: 2576
GIT1	NM_014030.2	GTGTATGACGAGGTGGATCGAAGAGAAAAT GATGCAGTGTGGCTGGCTACCCAAAACCACAGCACTCTGGT	SEQ ID NO: 2577
GJA1	NM_000165.2	GTTCACTGGGGGTGTATGGGGTAGATGGG TGGAGAGGGAGGGGATAAGAGAGGTGCATGTTGGTATTT	SEQ ID NO: 2578
GJB2	NM_004004.3	TGTCATGTACGACGGCTTCTCCATGCAGC GGCTGGTGAAGTGCAACGCCTGGCCTTGTCCCAACACTGTGGACT	SEQ ID NO: 2579
GPX1	NM_000581.2	GCTTATGACCGACCCCAAGCTCATCACC TGGTCTCCGGTGTGTCGCAACGATGTTGCCTGGAACTTT	SEQ ID NO: 2580
GPX2	NM_002083.1	CACACAGATCTCCTACTCCATCCAGTCCTGAGGAGCC TTAGGATGCAGCATGCCTTCAGGAGACACTGCTGGACC	SEQ ID NO: 2581
Grb10	NM_005311.2	CTTCGCCTTTGCTGATTGCCTCTCC AAACGCCTGCCTGACGACTGCCTTGGAGCATGTGCGTTATGG	SEQ ID NO: 2582
GRB14	NM_004490.1	TCCCACTGAAGCCCTTTCAGTTGCGGTTGAAGAAGG ACTCGCTTGGAGGAAAAAAGGATGTTTACGCCTGGGCACT	SEQ ID NO: 2583
GRB2	NM_002086.2	GTCCATCAGTGCATGACGTTTAAGGCCACGTATAGTCC TAGCTGACGCCAATAATAAAAAACAAGAAACCAAGTGGGCT	SEQ ID NO: 2584
GRB7	NM_005310.1	CCATCTGCATCCATCTTGTTTGGGCTCCCCA CCCTTGAGAAGTGCCTCAGATAATACCCTGGTGGCC	SEQ ID NO: 2585
GRIK1	NM_000830.2	GTTGGGTGCATCTCTCGGGCGTCCGGCAGCGGCTGTATC TCGGCATGAATTAAGAAGCTAGGAAGATGGAGCACG	SEQ ID NO: 2586
GRO1	NM_001511.1	CGAAAAGATGCTGAACAGTGACAAATCCAACTGACCAGA AGGGAGGAGGAAGCTCACTGGTGGCTGTTCCTGA	SEQ ID NO: 2587
GRP	NM_002091.1	CTGGGTCTCATAGAAGCAAAGGAGAACAGAAACCACCAGCCACCTC AACCCAAGGCCTTGGGCAATCAGCAGCCTTCGTGG	SEQ ID NO: 2588
GRPR	NM_005314.1	ATGCTGCTGGCCATTCCAGAGGCCGTGTTTTCTGACCTC CATCCCTTCCATGAGGAAAGCACCAACCAGACCT	SEQ ID NO: 2589
GSK3B	NM_002093.2	GACAAGGACGGCAGCAAGGTGACAACAGTGGTGGCA ACTCCTGGGCAGGGTCCAGACAGGCCACAA	SEQ ID NO: 2590
GSTA3	NM_000847.3	TCTCCAACTTCCCTCTGCTGAAGGCCCTGAAAACCAGA ATCAGCAACCTGCCCACGGTGAAGAAGT	SEQ ID NO: 2591
GSTM1	NM_000561.1	AAGCTATGAGGAAAAGAAGTACACGATGGGGGACGCTCCTGATTATGACAG AAGCCAGTGGCTGAATGAAAAATTCAAGCTGGGCC	SEQ ID NO: 2592
GSTM3	NM_000849.3	CAATGCCATCTTGCGCTACATCGCTCGCAAGCACAACAT GTGTGGTGAGACTGAAGAAGAAAAGATTCGAGTGGAC	SEQ ID NO: 2593
GSTp	NM_000852.2	GAGACCCTGCTGTCCCAGAACCAGGGAGGCAAGACCTTCATTGTGGGAGA CCAGATCTCCTTCGCTGACTACAACC	SEQ ID NO: 2594
GSTT1	NM_000853.1	CACCATCCCCACCCTGTCTTCCACAGCCGCCTGAAAGCC ACAATGAGAATGATGCACACTGAGGCC	SEQ ID NO: 2595
H2AFZ	NM_002106.2	CCGGAAAGGCCAAGACAAAGGCGGTTTCCCGCTCGCAGA GAGCCGGCTTGCAGTTCCCAGTGGGCCGTATT	SEQ ID NO: 2596

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
HB-EGF	NM_001945.1	GACTCCTTCGTCCCCAGTTGCCGTCTAGGATTGGGCCTCCCATAATTGCTTTGCCAAAATACCAGAGCCTTCAAGTGCCA	SEQ ID NO: 2597
hCRA a	U78556.1	TGACACCCTTACCTTCCTGAGAAATACCCCCTGGGAGCGCGGAAAGCAGAGCGGACAGGTCAGTGACTTCTATTTTTGACTCGTGTTTTT	SEQ ID NO: 2598
HDAC1	NM_004964.2	CAAGTACCACAGCGATGACTACATTAAATTCTTGCGCTCCATCCGTCCAGATAACATGTCGGAGTACAGCAAGC	SEQ ID NO: 2599
HDAC2	NM_001527.1	GGTGGCTACACAATCCGTAATGTTGCTCGATGTTGGACATATGAGACTGCAGTTGCCCTTGATTGTGAGATTCCCA	SEQ ID NO: 2600
HDGF	NM_004494.1	TCCTAGGCATTCTGGACCTCTGGGTTGGGATCAGGGGTAGGAATGGAAGGATGGAGCATCAACAGC	SEQ ID NO: 2601
hENT1	NM_004955.1	AGCCGTGACTGTTGAGGTCAAGTCCAGCATCGCAGGCAGCAGCACCTGGGAACGTTACTT	SEQ ID NO: 2602
Hepsin	NM_002151.1	AGGCTGCTGGAGGTCATCTCCGTGTGTGATTGCCCCAGAGGCCGTTTCTTGGCCGCCATCTGCCAAGACTGTGGCCGCAGGAAG	SEQ ID NO: 2603
HER2	NM_004448.1	CGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGAGTGTGCTATGGTCTGGGCATGGAGCACTTGCGAGAGG	SEQ ID NO: 2604
Herstatin	AF177761.2	CACCCTGTCCTATCCTTCCTCAGACCCTCTTGGGACCTAGTCTCTGCCTTCTACTCTCTACCCCTGGCC	SEQ ID NO: 2605
HES6	NM_018645.3	TTAGGGACCCTGCAGCTCTGGAGTGGGTGGAGGGAGGGAGCTACGGGCAGGAGGAAGAATTTTGTAG	SEQ ID NO: 2606
HGF	M29145.1	CCGAAATCCAGATGATGATGCTCATGGACCCTGGTGCTACACGGGAAATCCACTCATTCCTTGGG	SEQ ID NO: 2607
HIF1A	NM_001530.1	TGAACATAAAGTCTGCAACATGGAAGGTATTGCACTGCACAGGCCACATTCACGTATATGATACCAACAGTAACCAACCTCA	SEQ ID NO: 2608
HK1	NM_000188.1	TACGCACAGAGGCAAGCAGCTAAGAGTCCGGGATCCCCAGCCTACTGCCTCTCCAGCACTTCTCTC	SEQ ID NO: 2609
HLA-DPB1	NM_002121.4	TCCATGATGGTTCTGCAGGTTTCTGCGGCCCCCCGGACAGTGGCTCTGACGGCGTTACTGATGGTGCTGCTCA	SEQ ID NO: 2610
HLA-DRA	NM_019111.3	GACGATTTGCCAGCTTTGAGGCTCAAGGTGCATTGGCCAACATAGCTGTGGACAAAGCCAACCTGGA	SEQ ID NO: 2611
HLA-DRB1	NM_002124.1	GCTTTCTCAGGACCTGGTTGCTACTGGTTCGGCAACTGCAGAAAATGTCCTCCCTTGTGGCTTCCT	SEQ ID NO: 2612
HLA-G	NM_002127.2	CCTGCGCGGCTACTACAACCAGAGCGAGGCCAGTTCTCACACCCTCCAGTGGATGATTGGCTGCGACCTG	SEQ ID NO: 2613
HMGB1	NM_002128.3	TGGCCTGTCCATTGGTGATGTTGCGAAGAAACTGGGAGAGATGTGGAATAACACTGCTGCAGATGACAAGC	SEQ ID NO: 2614
hMLH	NM_000249.2	CTACTTCCAGCAACCCCAGAAAGAGACATCGGGAAGATTCTGATGTGGAAATGGTGGAAGATGATTCCCGAAAG	SEQ ID NO: 2615
HNRPAB	NM_004499.2	CAAGGGAGCGACCAACTGATCGCACACATGCTTTGTTTGGATATGGAGTGAACACAATTATGTACCAAATTTAACTTGGCAAAC	SEQ ID NO: 2616
HNRPD	NM_031370.2	GCCAGTAAGAACGAGGAGGATGAAGGCCATTCAAACTCCTCCCCACGACACTCTGAAGCAGCGACG	SEQ ID NO: 2617
HoxA1	NM_005522.3	AGTGACAGATGGACAATGCAAGAATGAACTCCTTCCTGGAATACCCCATACTTAGCAGTGGCGACTCGG	SEQ ID NO: 2618
HoxA5	NM_019102.2	TCCCTTGTGTTCCTTCTGTGAAGAAGCCCTGTTCTCGTTGCCCTAATTCATCTTTTAATCATGAGCCTGTTTATTGCC	SEQ ID NO: 2619
HOXB13	NM_006361.2	CGTGCCTTATGGTTACTTTGGAGGCGGGTACTACTCCTGCCGAGTGTCCCGGAGCTCGCTGAAACCCTGTG	SEQ ID NO: 2620
HOXB7	NM_004502.2	CAGCCTCAAGTTCGGTTTTCGCTACCGGAGCCTTCCCAGAACAAACTTCTTGTGCGTTTGCTTCCAAC	SEQ ID NO: 2621

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
HRAS	NM_005343.2	GGACGAATACGACCCCACTATAGAGGATTCCTACCG GAAGCAGGTGGTCATTGATGGGGAGACGTGC	SEQ ID NO: 2622
HSBP1	NM_001537.1	GGAGATGGCCGAGACTGACCCCAAGACCGTGCAGG ACCTCACCTCGGTGGTGCAGACACTCCTGCAG	SEQ ID NO: 2623
HSD17B1	NM_000413.1	CTGGACCGCACGGACATCCACACCTTCCACCGCTTCTACCA ATACCTCGCCCACAGCAAGCAAGTCTTTCGCGAGGCG	SEQ ID NO: 2624
HSD17B2	NM_002153.1	GCTTTCCAAGTGGGGAATTAAAGTTGCTTCCATCCA ACCTGGAGGCTTCCTAACAAATATCGCAGGCA	SEQ ID NO: 2625
HSPA1A	NM_005345.4	CTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTT GTCCCAAGGCTTCCCAGAGCGAACCTG	SEQ ID NO: 2626
HSPA1B	NM_005346.3	GGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTC CCAAGGCTTTCCAGAGCGAACCTGTGC	SEQ ID NO: 2627
HSPA4	NM_002154.3	TTCAGTGTGTCCAGTGCATCTTTAGTGGAGGTTCACAAG TCTGAGGAAAATGAGGAGCCAATGGAAACAGAT	SEQ ID NO: 2628
HSPA5	NM_005347.2	GGCTAGTAGAACTGGATCCCAACACCAAACTCTTAATTAGACCT AGGCCTCAGCTGCACTGCCCGAAAAGCATTTGGGCAGACC	SEQ ID NO: 2629
HSPA8	NM_006597.3	CCTCCCTCTGGTGGTGCTTCCTCAGGGCCCACCATTGA AGAGGTTGATTAAGCCAACCAAGTGTAGATGTAGC	SEQ ID NO: 2630
HSPB1	NM_001540.2	CCGACTGGAGGAGCATAAAAGCGCAGCCGAGCCCAGCGCCC CGCACTTTTCTGAGCAGACGTCCAGAGCAGAGTCAGCCAGCAT	SEQ ID NO: 2631
HSPCA	NM_005348.2	CAAAAGGCAGAGGCTGATAAGAACGACAAGTCTGTGAAG GATCTGGTCATCTTGCTTTATGAAACTGCGCT	SEQ ID NO: 2632
HSPE1	NM_002157.1	GCAAGCAACAGTAGTCGCTGTTGGATCGGGTTCTAAAGGAA AGGGTGGAGAGATTCAACCAGTTAGCGTGAAAGTTGG	SEQ ID NO: 2633
HSPG2	NM_005529.2	GAGTACGTGTGCCGAGTGTTGGGCAGCTCCGTGCCT CTAGAGGCCTCTGTCCTGGTCACCATTGAG	SEQ ID NO: 2634
ICAM1	NM_000201.1	GCAGACAGTGACCATCTACAGCTTTCCGGCGCCCAACGTGAT TCTGACGAAGCCAGAGGTCTCAGAAG	SEQ ID NO: 2635
ICAM2	NM_000873.2	GGTCATCCTGACACTGCAACCCACTTTGGTGGCTGT GGGCAAGTCCTTCACCATTGAGTGCA	SEQ ID NO: 2636
ID1	NM_002165.1	AGAACCGCAAGGTGAGCAAGGTGGAGATTCTCCAGCAC GTCATCGACTACATCAGGGACCTTCAGTTGGA	SEQ ID NO: 2637
ID2	NM_002166.1	AACGACTGCTACTCCAAGCTCAAGGAGCTGGTGCC CAGCATCCCCCAGAACAAGAAGGTGAGCAAGATGGAAATCC	SEQ ID NO: 2638
ID3	NM_002167.2	CTTCACCAAATCCCTTCCTGGAGACTAAACCTGGTGCTCAGGA GCGAAGGACTGTGAACTTGTAGCCTGAAGAGCCAGAG	SEQ ID NO: 2639
ID4	NM_001546.2	TGGCCTGGCTCTTAATTTGCTTTTGTTTTGCCCAGTATAGACTCGGA AGTAAGAGTTATAGCTAGTGGTCTTGCATGATTGCA	SEQ ID NO: 2640
IFIT1	NM_001548.1	TGACAACCAAGCAAATGTGAGGAGTCTGGTGACCTGGGGCAAC TTTGCCTGGATGTATTACCACATGGGCAGACTG	SEQ ID NO: 2641
IGF1	NM_000618.1	TCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGC ACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCG	SEQ ID NO: 2642
IGF1R	NM_000875.2	GCATGGTAGCCGAAGATTTCACAGTCAAAATCGGAGATTTTGGTA TGACGCGAGATATCTATGAGACAGACTATTACCGGAAA	SEQ ID NO: 2643
IGF2	NM_000612.2	CCGTGCTTCCGGACAACTTCCCCAGATACCCCGTGGGCAAGT TCTTCCAATATGACACCTGGAAGCAGTCCA	SEQ ID NO: 2644
IGFBP2	NM_000597.1	GTGGACAGCACCATGAACATGTTGGGCGGGGGAGGCAGTG CTGGCCGGAAGCCCCTCAAGTCGGGTATGAAGG	SEQ ID NO: 2645
IGFBP3	NM_000598.1	ACGCACCGGGTGTCTGATCCCAAGTTCCACCCCCTC CATTCAAAGATAATCATCATCAAGAAAGGGCA	SEQ ID NO: 2646

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
IGFBP5	NM_000599.1	TGGACAAGTACGGGATGAAGCTGCCAGGCATGGAGTACGTTGACGGGGACTTTCAGTGCCACACCTTCG	SEQ ID NO: 2647
IGFBP6	NM_002178.1	TGAACCGCAGAGACCAACAGAGGAATCCAGGCACCTCTACCACGCCCTCCCAGCCCAATTCTGCGGGTGTCCAAGAC	SEQ ID NO: 2648
IGFBP7	NM_001553	GGGTCACTATGGAGTTCAAAGGACAGAACTCCTGCCTGGTGACCGGGACAACCTGGCCATTCAGACCC	SEQ ID NO: 2649
IHH	NM_002181.1	AAGGACGAGGAGAACACAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCT	SEQ ID NO: 2650
IL-8	NM_000584.2	AAGGAACCATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGCCTTCCTGAT	SEQ ID NO: 2651
IL10	NM_000572.1	GGCGCTGTCATCGATTTCTTCCCTGTGAAAACAAGAGCAAGGCCGTGGAGCAGGTGAAGAATGCCTTTAATAAGCTCCA	SEQ ID NO: 2652
IL1B	NM_000576.2	AGCTGAGGAAGATGCTGGTTCCCTGCCCACAGACCTTCCAGGAGAATGACCTGAGCACCTTCTTTCC	SEQ ID NO: 2653
IL6	NM_000600.1	CCTGAACCTTCCAAAGATGGCTGAAAAAGATGGATGCTTCCAATCTGGATTCAATGAGGAGACTTGCCTGGT	SEQ ID NO: 2654
IL6ST	NM_002184.2	GGCCTAATGTTCCAGATCCTTCAAAGAGTCATATTGCCCAGTGGTCACCTCACACTCCTCCAAGGCACAATTTT	SEQ ID NO: 2655
ILT-2	NM_006669.1	AGCCATCACTCTCAGTGCAGCCAGGTCCTATCGTGGCCCCTGAGGAGACCCTGACTCTGCAGT	SEQ ID NO: 2656
IMP-1	NM_006546.2	GAAAGTGTTTGCGGAGCACAAGATCTCCTACAGCGGCCAGTTCTTGGTCAAATCCGGCTACGCCTTC	SEQ ID NO: 2657
IMP2	NM_006548.3	CAATCTGATCCCAGGGTTGAACCTCAGCGCACTTGGCATCTTTTCAACAGGACTGTCCGTGCTATCTCCACCAGCAGGGCC	SEQ ID NO: 2658
ING1L	NM_001564.1	TGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA	SEQ ID NO: 2659
ING5	NM_032329.4	CCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATG	SEQ ID NO: 2660
INHA	NM_002191.2	CCTCCCAGTTTCATCTTCCACTACTGTCATGGTGGTTGTGGGCTGCAGATCCCACCAAACCTGTCCCTTCCAGTCCCT	SEQ ID NO: 2661
INHBA	NM_002192.1	GTGCCCGAGCCATATAGCAGGCACGTCCGGGTCCTCACTGTCCTTCCACTCAACAGTCATCAACCACTACCG	SEQ ID NO: 2662
INHBB	NM_002193.1	AGCCTCCAGGATACCAGCAAATGGATGCGGTGACAAATGGCAGCTTAGCTACAAATGCCTGTCAGTCGGAGA	SEQ ID NO: 2663
IRS1	NM_005544.1	CCACAGCTCACCTTCTGTCAGGTGTCCATCCCAGCTCCAGCCAGCTCCCAGAGAGGAAGAGACTGGCACTGAGG	SEQ ID NO: 2664
ITGA3	NM_002204.1	CCATGATCCTCACTCTGCTGGTGGACTATACACTCCAGACCTCGCTTAGCATGGTAAATCACCGGCTACAAAGCTTC	SEQ ID NO: 2665
ITGA4	NM_000885.2	CAACGCTTCAGTGATCAATCCCGGGGCGATTTACAGATGCAGGATCGGAAAGAATCCCGGCCAGAC	SEQ ID NO: 2666
ITGA5	NM_002205.1	AGGCCAGCCCTACATTATCAGAGCAAGAGCCGGATAGAGGACAAGGCTCAGATCTTGCTGGACTGTGGAGAAGAC	SEQ ID NO: 2667
ITGA6	NM_000210.1	CAGTGACAAACAGCCCTTCCAACCCAAGGAATCCCACAAAAGATGGCGATGACGCCCATGAGGCTAAAC	SEQ ID NO: 2668
ITGA7	NM_002206.1	GATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCT	SEQ ID NO: 2669
ITGAV	NM_002210.2	ACTCGGACTGCACAAGCTATTTTTGATGACAGCTATTTGGGTTATTCTGTGGCTGTCGGAGATTTCAATGGTGATGGCA	SEQ ID NO: 2670
ITGB1	NM_002211.2	TCAGAATTGGATTTGGCTCATTTGTGGAAAAGACTGTGATGCCTTACATTAGCACAACACCAGCTAAGCTCAGG	SEQ ID NO: 2671

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Gene	Locus Link	Sequence	Sequence ID Number
ITGB3	NM_000212.1	ACCGGGAGCCCTACATGACCGAAAATACCTGCAACCGTTACTGCCGTGACGAGATTGAGTCAGTGAAAGAGCTTAAGG	SEQ ID NO: 2672
ITGB4	NM_000213.2	CAAGGTGCCCTCAGTGGAGCTCACCAACCTGTACCCGTATTGCGACTATGAGATGAAGGTGTGCGC	SEQ ID NO: 2673
ITGB5	NM_002213.3	TCGTGAAAGATGACCAGGAGGCTGTGCTATGTTTCTACAAAACCGCCAAGGACTGCGTCATGATGTTCACC	SEQ ID NO: 2674
K-ras	NM_033360.2	GTCAAAATGGGGAGGGACTAGGGCAGTTTGGATAGCTCAACAAGATACAATCTCACTCTGTGGTGGTCCTG	SEQ ID NO: 2675
KCNH2 iso a/b	NM_000238.2	GAGCGCAAAGTGGAAATCGCCTTCTACCGGAAAGATGGGAGCTGCTTCCTATGTCTGGTGGATGTGGTGCCCGTGAAGA	SEQ ID NO: 2676
KCNH2 iso a/c	NM_172057.1	TCCTGCTGCTGGTCATCTACACGGCTGTCTTCACACCCTACTCGGCTGCCTTCCTGCTGAAGGAGACGGAAGAAGG	SEQ ID NO: 2677
KCNK4	NM_016611.2	CCTATCAGCCGCTGGTGTGGTTCTGGATCCTGCTCGGCCTGGCTTACTTCGCCTCAGTGCTCACCACCA	SEQ ID NO: 2678
KDR	NM_002253.1	GAGGACGAAGGCCTCTACACCTGCCAGGCATGCAGTGTTCTTGGCTGTGCAAAAGTGGAGGCATTTTT	SEQ ID NO: 2679
Ki-67	NM_002417.1	CGGACTTTGGGTGCGACTTGACGAGCGGTGGTTCGACAAGTGGCCTTGCGGGCCGGATCGTCCCAGTGGAAGAGTTGTAA	SEQ ID NO: 2680
KIAA0125	NM_014792.2	GTGTCCTGGTCCATGTGGTGCACGTGTCTCCACCTCCAAGGAGAGGCTCCTCAGTGTGCACCTCCC	SEQ ID NO: 2681
KIF22	NM_007317.1	CTAAGGCACTTGCTGGAAGGGCAGAATGCCAGTGTGCTTGCCTATGGACCCACAGGAGCTGGGAAGA	SEQ ID NO: 2682
KIF2C	NM_006845.2	AATTCCTGCTCCAAAAGAAAGTCTTCGAAGCCGCTCCACTCGCATGTCCACTGTCTCAGAGCTTCGCATCACG	SEQ ID NO: 2683
KIFC1	XM_371813.1	CCACAGGGTTGAAGAACCAGAAGCCAGTTCCTGCTGTTCCTGTCCAGAAGTCTGGCACATCAGGTG	SEQ ID NO: 2684
Kitlng	NM_000899.1	GTCCCCGGGATGGATGTTTTGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATC	SEQ ID NO: 2685
KLF5	NM_001730.3	GTGCAACCGCAGCTTCTCGCGCTCTGACCACCTGGCCCTGCATATGAAGAGGCACCAGAACTGAGCACTGCCCG	SEQ ID NO: 2686
KLF6	NM_001300.4	CACGAGACCGGCTACTTCTCGGCGCTGCCGTCTCTGGAGGAGTACTGGCAACAGACCTGCCTAGAGC	SEQ ID NO: 2687
KLK10	NM_002776.1	GCCCAGAGGCTCCATCGTCCATCCTCTTCCTCCCCAGTCGGCTGAACTCTCCCCTTGTCTGCACTGTTCAAACCTCTG	SEQ ID NO: 2688
KLK6	NM_002774.2	GACGTGAGGGTCCTGATTCTCCCTGGTTTTACCCCAGCTCCATCCTTGCATCACTGGGGAGGACGTGATGAGTGAGGA	SEQ ID NO: 2689
KLRK1	NM_007360.1	TGAGAGCCAGGCTTCTTGTATGTCTCAAAATGCCAGCCTTCTGAAAGTATACAGCAAAGAGGACCAGGAT	SEQ ID NO: 2690
KNTC2	NM_006101.1	ATGTGCCAGTGAGCTTGAGTCCTTGGAGAAACACAAGCACCTGCTAGAAAGTACTGTTAACCAGGGGCTCA	SEQ ID NO: 2691
KRAS2	NM_004985.3	GAGACCAAGGTTGCAAGGCCAGGCCCTGTGTGAACCTTTGAGCTTTCATAGAGAGTTTCACAGCATGGACTG	SEQ ID NO: 2692
KRT19	NM_002276.1	TGAGCGGCAGAATCAGGAGTACCAGCGGCTCATGGACATCAAGTCGCGGCTGGAGCAGGAGATTGCCACCTACCGCA	SEQ ID NO: 2693
KRT8	NM_002273.1	GGATGAAGCTTACATGAACAAGGTAGAGCTGGAGTCTCGCCTGGAAGGGCTGACCGACGAGATCAACTTCCTCAGGCAGCTATATG	SEQ ID NO: 2694
LAMA3	NM_000227.2	CAGATGAGGCACATGGAGACCCAGGCCAAGGACCTGAGGAATCAGTTGCTCAACTACCGTTCTGCCATTTCAA	SEQ ID NO: 2695
LAMB3	NM_000228.1	ACTGACCAAGCCTGAGACCTACTGCACCCAGTATGGCGAGTGGCAGATGAAATGCTGCAAGTGTGAC	SEQ ID NO: 2696

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
LAMC2	NM_005562.1	ACTCAAGCGGAAATTGAAGCAGATAGGTCTTATCAGCACAGTCTCCGCCTCCTGGATTCAGTGTCTCGGCTTCAGGGAGT	SEQ ID NO: 2697
LAT	NM_014387.2	GTGAACGTTCCGGAGAGCGGGGAGAGCGCAGAAGCGTCTCTGGATGGCAGCCGGGAGTATGTGAATGT	SEQ ID NO: 2698
LCN2	NM_005564.2	CGCTGGGCAACATTAAGAGTTACCCTGGATTAACGAGTTACCTCGTCCGAGTGGTGAGCACCAACTACAACCAGCATGCT	SEQ ID NO: 2699
LDLRAP1	NM_015627.1	CAGTGCCTCTCGCCTGTCGACTGGGACAAGCCTGACAGCAGCGGCACAGAGCAGGATGACCTCTTCA	SEQ ID NO: 2700
LEF	NM_016269.2	GATGACGGAAAGCATCCAGATGGAGGCCTCTACAACAAGGGACCCTCCTACTCGAGTTATTCCGGG	SEQ ID NO: 2701
LGALS3	NM_002306.1	AGCGGAAAATGGCAGACAATTTTTCGCTCCATGATGCGTTATCTGGGTCTGGAAACCCAAACCCTCAAG	SEQ ID NO: 2702
LGMN	NM_001008530.1	TTGGTGCCGTTCCTATAGATGATCCTGAAGATGGAGGCAAGCACTGGGTGGTGATCGTGGCAGGTTC	SEQ ID NO: 2703
LILRB3	NM_006864.1	CACCTGGTCTGGGAAGATACCTGGAGGTTTTGATTGGGGTCTCGGTGGCCTTCGTCCTGCTGCTCTT	SEQ ID NO: 2704
LMNB1	NM_005573.1	TGCAAACGCTGGTGTCACAGCCAGCCCCCCAACTGACCTCATCTGGAAGAACCAGAACTCGTGGGG	SEQ ID NO: 2705
LMYC	NM_012421.1	CCCATCCAGAACACTGATTGCTGTCATTCAAGTGAAAGGGATGGAGGTCAGAAAGGGTGCATAGAAAGCAG	SEQ ID NO: 2706
LOX	NM_002317.3	CCAATGGGAGAACAACGGGCAGGTGTTCAGCTTGCTGAGCCTGGGCTCACAGTACCAGCCTCAGCG	SEQ ID NO: 2707
LOXL2	NM_002318.1	TCAGCGGGCTCTTAAACAACCAGCTGTCCCCGCAGTAAAGAAGCCTGCGTGGTCAACTCCTGTCTT	SEQ ID NO: 2708
LRP5	NM_002335.1	CGACTATGACCCACTGGACAAGTTCATCTACTGGGTGGATGGGCGCCAGAACATCAAGCGAGCCAAG	SEQ ID NO: 2709
LRP6	NM_002336.1	GGATGTAGCCATCTCTGCCTCTATAGACCTCAGGGCCTTCGCTGTGCTTGCCCTATTGGCTTTGAACT	SEQ ID NO: 2710
LY6D	NM_003695.2	AATGCTGATGACTTGGAGCAGGCCCCACAGACCCCACAGAGGATGAAGCCACCCCACAGAGGATGCAG	SEQ ID NO: 2711
MAD	NM_002357.1	TGGTTCTGATTAGGTAACGTATTGGACCTGCCCACAACTCCCTTGCACGTAAACTTCAGTGTCCCACCTTGACC	SEQ ID NO: 2712
MAD1L1	NM_003550.1	AGAAGCTGTCCCTGCAAGAGCAGGATGCAGCGATTGTGAAGAACATGAAGTCTGAGCTGGTACGGCT	SEQ ID NO: 2713
MAD2L1	NM_002358.2	CCGGGAGCAGGGAATCACCCTGCGCGGGAGCGCCGAAATCGTGGCCGAGTTCTTCTCATTCGGCATCAACAGCAT	SEQ ID NO: 2714
MADH2	NM_005901.2	GCTGCCTTTGGTAAGAACATGTCGTCCATCTTGCCATTCACGCCGCCAGTTGTGAAGAGACTGCTGGGAT	SEQ ID NO: 2715
MADH4	NM_005359.3	GGACATTACTGGCCTGTTCACAATGAGCTTGCATTCCAGCCTCCCATTTCCAATCATCCTGCTCCTGAGTATTGGT	SEQ ID NO: 2716
MADH7	NM_005904.1	TCCATCAAGGCTTTCGACTACGAGAAGGCGTACAGCCTGCAGCGGCCCAATGACCACGAGTTTATGCAGCAG	SEQ ID NO: 2717
MAP2	NM_031846.1	CGGACCACCAGGTCAGAGCCAATTCGCAGAGCAGGGAAGAGTGGTACCTCAACACCCACTACCCCTG	SEQ ID NO: 2718
MAP2K1	NM_002755.2	GCCTTTCTTACCCAGAAGCAGAAGGTGGGAGAACTGAAGGATGACGACTTTGAGAAGATCAGTGAGCTGGGGGCTG	SEQ ID NO: 2719
MAP3K1	XM_042066.8	GGTTGGCATCAAAAGGAACTGGTGCAGGAGAGTTTCAGGGACAATTACTGGGGACAATTGCATTTATGGCA	SEQ ID NO: 2720
MAPK14	NM_139012.1	TGAGTGGAAAAGCCTGACCTATGATGAAGTCATCAGCTTTGTGCCACCACCCCTTGACCAAGAAGAGATGGAGTCC	SEQ ID NO: 2721

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
Maspin	NM_002639.1	CAGATGGCCACTTTGAGAACATTTTAGCTGACAACAGTGTGAACGACCAGACCAAAATCCTTGTGGTTAATGCTGCC	SEQ ID NO: 2722
MAX	NM_002382.3	CAAACGGGCTCATCATAATGCACTGGAACGAAAACGTAGGGACCACATCAAAGACAGCTTTCACAGTTTGCGGGA	SEQ ID NO: 2723
MCM2	NM_004526.1	GACTTTTGCCCGCTACCTTTCATTCCGGCGTGACAACAATGAGCTGTTGCTCTTCATACTGAAGCAGTTAGTGGC	SEQ ID NO: 2724
MCM3	NM_002388.2	GGAGAACAATCCCCTTGAGACAGAATATGGCCTTTCTGTCTACAAGGATCACCAGACCATCACCATCCAGGAGAT	SEQ ID NO: 2725
MCM6	NM_005915.2	TGATGGTCCTATGTGTCACATTCATCACAGGTTTCATACCAACACAGGCTTCAGCACTTCCTTTGGTGTGTTTCCTGTCCCA	SEQ ID NO: 2726
MCP1	NM_002982.1	CGCTCAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATCTCAGTGC	SEQ ID NO: 2727
MDK	NM_002391.2	GGAGCCGACTGCAAGTACAAGTTTGAGAACTGGGGTGCGTGTGATGGGGGCACAGGCACCAAAGTC	SEQ ID NO: 2728
MDM2	NM_002392.1	CTACAGGGACGCCATCGAATCCGGATCTTGATGCTGGTGTAAGTGAACATTCAGGTGATTGGTTGGAT	SEQ ID NO: 2729
MGAT5	NM_002410.2	GGAGTCGAAGGTGGACAATCTTGTTGTCAATGGCACCGGAACAAACTCAACCAACTCCACTACAGCTGTTCCCA	SEQ ID NO: 2730
MGMT	NM_002412.1	GTGAAATGAAACGCACCACACTGGACAGCCCTTTGGGGAAGCTGGAGCTGTCTGGTTGTGAGCAGGGTC	SEQ ID NO: 2731
mGST1	NM_020300.2	ACGGATCTACCACACCATTGCATATTTGACACCCCTTCCCCAGCCAAATAGAGCTTTGAGTTTTTTTGTTGGATATGGA	SEQ ID NO: 2732
MMP1	NM_002421.2	GGGAGATCATCGGGACAACTCTCCTTTTGATGGACCTGGAGGAAATCTTGCTCATGCTTTTCAACCAGGCCC	SEQ ID NO: 2733
MMP12	NM_002426.1	CCAACGCTTGCCAAATCCTGACAATTCAGAACCAGCTCTCTGTGACCCCAATTTGAGTTTTGATGCTGTCACTACCGT	SEQ ID NO: 2734
MMP2	NM_004530.1	CCATGATGGAGAGGCAGACATCATGATCAACTTTGGCCGCTGGGAGCATGGCGATGGATACCCCTTTGACGGTAAGGACGGACTCC	SEQ ID NO: 2735
MMP7	NM_002423.2	GGATGGTAGCAGTCTAGGGATTAACTTCCTGTATGCTGCAACTCATGAACTTGGCCATTCTTTGGGTATGGGACATTCC	SEQ ID NO: 2736
MMP9	NM_004994.1	GAGAACCAATCTCACCGACAGGCAGCTGGCAGAGGAATACCTGTACCGCTATGGTTACACTCGGGTG	SEQ ID NO: 2737
MRP1	NM_004996.2	TCATGGTGCCCGTCAATGCTGTGATGGCGATGAAGACCAAGACGTATCAGGTGGCCCACATGAAGAGCAAAGACAATCG	SEQ ID NO: 2738
MRP2	NM_000392.1	AGGGGATGACTTGGACACATCTGCCATTCGACATGACTGCAATTTTGACAAAGCCATGCAGTTTT	SEQ ID NO: 2739
MRP3	NM_003786.2	TCATCCTGGCGATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGCTGGAGTCGCTTTCATGGTCTTGCTGATTCCACTCAACGG	SEQ ID NO: 2740
MRP4	NM_005845.1	AGCGCCTGGAATCTACAACTCGGAGTCCAGTGTTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCT	SEQ ID NO: 2741
MRPL40	NM_003776.2	ACTTGCAGGCTGCTATCCTTAACATGCTGCCCCTGAGAGTAGGAATGACCAGGGTTCAAGTCTGCT	SEQ ID NO: 2742
MSH2	NM_000251.1	GATGCAGAATTGAGGCAGACTTTACAAGAAGATTTACTTCGTCGATTCCCAGATCTTAACCGACTTGCCAAGA	SEQ ID NO: 2743
MSH3	NM_002439.1	TGATTACCATCATGGCTCAGATTGGCTCCTATGTTCCTGCAGAAGAAGCGACAATTGGGATTGTGGATGGCATTTTCACAAG	SEQ ID NO: 2744
MSH6	NM_000179.1	TCTATTGGGGGATTGGTAGGAACCGTTACCAGCTGGAAATTCCTGAGAATTTCACCACTCGCAATTTG	SEQ ID NO: 2745
MT3	NM_005954.1	GTGTGAGAAGTGTGCCAAGGACTGTGTGTGCAAAGGCGGAGAGGCAGCTGAGGCAGAAGCAGAGAAGTGCAG	SEQ ID NO: 2746

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
MTA1	NM_004689.2	CCGCCCTCACCTGAAGAGAAACGCGCTCCTTGGCGGACACTGGGGGAGGAGAGGAAGAAGCGCGGCTAACTTATTCC	SEQ ID NO: 2747
MUC1	NM_002456.1	GGCCAGGATCTGTGGTGGTACAATTGACTCTGGCCTTCCGAGAAGGTACCATCAATGTCCACGACGTGGAG	SEQ ID NO: 2748
MUC2	NM_002457.1	CTATGAGCCATGTGGGAACCGGAGCTTCGAGACCTGCAGGACCATCAACGGCATCCACTCCAACAT	SEQ ID NO: 2749
MUC5B	XM_039877.11	TGCCCTTGCACTGTCCTAACGGCTCAGCCATCCTGCACACCTACACCCACGTGGATGAGTGTGGCTG	SEQ ID NO: 2750
MUTYH	NM_012222.1	GTACGACCAAGAGAAACGGGACCTACCATGGAGAAGACGGGCAGAAGATGAGATGGACCTGGACAGG	SEQ ID NO: 2751
MVP	NM_017458.1	ACGAGAACGAGGGCATCTATGTGCAGGATGTCAAGACCGGAAAGGTGCGCGCTGTGATTGGAAGCACCTACATGC	SEQ ID NO: 2752
MX1	NM_002462.2	GAAGGAATGGGAATCAGTCATGAGCTAATCACCCTGGAGATCAGCTCCCGAGATGTCCCGGATCTGACTCTAATAGAC	SEQ ID NO: 2753
MXD4	NM_006454.2	AGAAACTGGAGGAGCAGGACCGCCGGGCACTGAGCATCAAGGAGCAGCTGCAGCAGGAGCATCGTTTCCTGAAG	SEQ ID NO: 2754
MYBL2	NM_002466.1	GCCGAGATCGCCAAGATGTTGCCAGGGAGGACAGACAATGCTGTGAAGAATCACTGGAACTCTACCATCAAAAG	SEQ ID NO: 2755
MYH11	NM_002474.1	CGGTACTTCTGAGGGCTAATATATACGTACTCTGGCCTCTTCTGCGTGGTGGTCAACCCCTATAAACACCTGCCCATCTACTCGG	SEQ ID NO: 2756
MYLK	NM_053025.1	TGACGGAGCGTGAGTGCATCAAGTACATGCGGCAGATCTCGGAGGGAGTGGAGTACATCCACAAGCAGGGCAT	SEQ ID NO: 2757
NAD2	NM_000015.1	TAACTGACATTCTTGAGCACCAGATCCGGGCTGTTCCCTTTGAGAACCTTAACATGCATTGTGGGCAAGCCAT	SEQ ID NO: 2758
NAV2	NM_182964.3	CTCTCCCAGCACAGCTTGAACCTCACTGAGTCAACCAGCCTGGACATGTTGCTGGATGACACTGGTG	SEQ ID NO: 2759
NCAM1	NM_000615.1	TAGTTCCCAGCTGACCATCAAAAAGGTGGATAAGAACGACGAGGCTGAGTACATCTGCATTGCTGAGAACAAGGCTG	SEQ ID NO: 2760
NDE1	NM_017668.1	CTACTGCGGAAAGTCGGGGCACTGGAGTCCAAACTCGCTTCCTGCCGGAACCTCGTGTACGATCAGTCC	SEQ ID NO: 2761
NDRG1	NM_006096.2	AGGGCAACATTCCACAGCTGCCCTGGCTGTGATGAGTGTCCTTGCAGGGGCCGGAGTAGGAGCACTG	SEQ ID NO: 2762
NDUFS3	NM_004551.1	TATCCATCCTGATGGCGTCATCCCAGTGCTGACTTTCCTCAGGGATCACACCAATGCACAGTTCAA	SEQ ID NO: 2763
NEDD8	NM_006156.1	TGCTGGCTACTGGGTGTTAGTTTGCAGTCCTGTGTGCTTCCCTCTCTTATGACTGTGTCCCTGGTTGTC	SEQ ID NO: 2764
NEK2	NM_002497.1	GTGAGGCAGCGCGACTCTGGCGACTGGCCGGCCATGCCTTCCCGGGCTGAGGACTATGAAGTGTTGTACACCATTGGCA	SEQ ID NO: 2765
NF2	NM_000268.2	ACTCCAGAGCTGACCTCCACCGCCCAGCCTGGGAAGTCATTGTAGGGAGTGAGACACTGAAGCCCTGA	SEQ ID NO: 2766
NFKBp50	NM_003998.1	CAGACCAAGGAGATGGACCTCAGCGTGGTGCGGCTCATGTTTACAGCTTTTCTTCCGGATAGCACTGGCAGCT	SEQ ID NO: 2767
NFKBp65	NM_021975.1	CTGCCGGGATGGCTTCTATGAGGCTGAGCTCTGCCCGGACCGCTGCATCCACAGTTTCCAGAACCTGG	SEQ ID NO: 2768
NISCH	NM_007184.1	CCAAGGAATCATGTTCGTTCAGGAGGAGGCCCTGGCCAGCAGCCTCTCGTCCACTGACAGTCTGACTCCCGAGCACCA	SEQ ID NO: 2769
Nkd-1	NM_033119.3	GAGAGAGTGAGCGAACCCTGCCCAGGCTCCAAGAAGCAGCTGAAGTTTGAAGAGCTCCAGTGCGACG	SEQ ID NO: 2770
NMB	NM_021077.1	GGCTGCTGGTACAAATACTGCAGAAATGACACCAATAATAGGGGCAGACACAACAGCGTGGCTTAGATTG	SEQ ID NO: 2771

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
NMBR	NM_002511.1	TGATCCATCTCTAGGCCACATGATTGTCACCTTAGTTGCCCGGG TTCTCAGTTTTGGCAATTCTTGTGTCAACCCATTTGCTC	SEQ ID NO: 2772
NME1	NM_000269.1	CCAACCCTGCAGACTCCAAGCCTGGGACCATCCGTGG AGACTTCTGCATACAAGTTGGCAGGAACATTATACAT	SEQ ID NO: 2773
NOS3	NM_000603.2	ATCTCCGCCTCGCTCATGGGCACGGTGATGGCGAAGC GAGTGAAGGCGACAATCCTGTATGGCTCCGA	SEQ ID NO: 2774
NOTCH1	NM_017617.2	CGGGTCCACCAGTTTGAATGGTCAATGCGAGTGGCTGT CCCGGCTGCAGAGCGGCATGGTGCCGAACCAATACAAC	SEQ ID NO: 2775
NOTCH2	NM_024408.2	CACTTCCCTGCTGGGATTATATCAACAACCAGTG TGATGAGCTGTGCAACACGGTCGAGTGCCTGTTTGACAACT	SEQ ID NO: 2776
NPM1	NM_002520.2	AATGTTGTCCAGGTTCTATTGCCAAGAATGTGTTGTCCAAA ATGCCTGTTTAGTTTTTAAAGATGGAACTCCACCCTTTGCTTG	SEQ ID NO: 2777
NR4A1	NM_002135.2	CACAGCTTGCTTGTCGATGTCCCTGCCTTCGCCTG CCTCTCTGCCCTTGTCCTCATCACCGACCGGCAT	SEQ ID NO: 2778
NRG1	NM_013957.1	CGAGACTCTCCTCATAGTGAAAGGTATGTGTCAGCCATGACCAC CCCGGCTCGTATGTCACCTGTAGATTTCCACACGCCAAG	SEQ ID NO: 2779
NRP1	NM_003873.1	CAGCTCTCTCCACGCGATTCATCAGGATCTACCCCGAGAGAGCCACT CATGGCGGACTGGGGCTCAGAATGGAGCTGCTGGG	SEQ ID NO: 2780
NRP2	NM_003872.1	CTACAGCCTAAACGGCAAGGACTGGGAATACATTCA GGACCCCAGGACCCAGCAGCCAAAGCTGTTCGAAGGGAAC	SEQ ID NO: 2781
NTN1	NM_004822.1	AGAAGGACTATGCCGTCCAGATCCACATCCTGAAGG CGGACAAGGCGGGGGACTGGTGGAAGTTCACGG	SEQ ID NO: 2782
NUFIP1	NM_012345.1	GCTTCCACATCGTGGTATTGGAGACAGTCTTCTGATAGGTTTCCT CGGCATCAGAAGTCCTTCAACCCTGCAGTT	SEQ ID NO: 2783
ODC1	NM_002539.1	AGAGATCACCGGCGTAATCAACCCAGCGTTGGACAAATACTTTC CGTCAGACTCTGGAGTGAGAATCATAGCTGAGCCCG	SEQ ID NO: 2784
OPN, osteopontin	NM_000582.1	CAACCGAAGTTTTCACTCCAGTTGTCCCCACAGTAGACACAT ATGATGGCCGAGGTGATAGTGTGGTTTATGGACTGAGG	SEQ ID NO: 2785
ORC1L	NM_004153.2	TCCTTGACCATACCGGAGGGTGCATGTACATCTCCGG TGTCCCTGGGACAGGGAAGACTGCCACTG	SEQ ID NO: 2786
OSM	NM_020530.3	GTTTCTGAAGGGGAGGTCACAGCCTGAGCTGGC CTCCTATGCCTCATCATGTCCCAAACCAGACACCT	SEQ ID NO: 2787
OSMR	NM_003999.1	GCTCATCATGGTCATGTGCTACTTGAAAAGTCAGTGGATCAA GGAGACCTGTTATCCTGACATCCCTGACCCTTACA	SEQ ID NO: 2788
P14ARF	S78535.1	CCCTCGTGCTGATGCTACTGAGGAGCCAGCGTCTAGGGCAGCAG CCGCTTCCTAGAAGACCAGGTCATGATG	SEQ ID NO: 2789
p16-INK4	L27211.1	GCGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACCAGAGA GGCTCTGAGAAACCTCGGGAAACTTAGATCATCA	SEQ ID NO: 2790
p21	NM_000389.1	TGGAGACTCTCAGGGTCGAAAACGGCGGCAGA CCAGCATGACAGATTTCTACCACTCCAAACGCC	SEQ ID NO: 2791
p27	NM_004064.1	CGGTGGACCACGAAGAGTTAACCCGGGACTT GGAGAAGCACTGCAGAGACATGGAAGAGGCGAGCC	SEQ ID NO: 2792
P53	NM_000546.2	CTTTGAACCCTTGCTTGCAATAGGTGTGCGTC AGAAGCACCCAGGACTTCCATTTGCTTTGTCCCGGG	SEQ ID NO: 2793
p53R2	AB036063.1	CCCAGCTAGTGTTCCTCAGAACAAAGATTGGAAAAAGCTGGCCGAG AACCATTTATACATAGAGGAAGGGCTTACGG	SEQ ID NO: 2794
PADI4	NM_012387.1	AGCAGTGGCTTGCTTTCTTCTCCTGTGATGTCCCA GTTTCCCACTCTGAAGATCCCAACATGGTCCTAGCA	SEQ ID NO: 2795
PAI1	NM_000602.1	CCGCAACGTGGTTTTCTCACCCTATGGGGTGGCCTCG GTGTTGGCCATGCTCCAGCTGACAACAGGAGGAGAAACCCAGCA	SEQ ID NO: 2796

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
Pak1	NM_002576.3	GAGCTGTGGGTTGTTATGGAATACTTGGCTGGAGGCTCCTTGACAGATGTGGTGACAGAAACTTGCATGG	SEQ ID NO: 2797
PARC	NM_015089.1	GGAGCTGACCTGCTTCCTACATCGCCTGGCCTCGATGCATAAGGACTATGCTGTGGTGCTCTGCT	SEQ ID NO: 2798
PCAF	NM_003884.3	AGGTGGCTGTGTTACTGCAACGTGCCACAGTTCTGCGACAGTCTACCTCGGTACGAAACCACACAGGTG	SEQ ID NO: 2799
PCNA	NM_002592.1	GAAGGTGTTGGAGGCACTCAAGGACCTCATCAACAGGCCTGCTGGGATATTAGCTCCAGCGGTGTAAACC	SEQ ID NO: 2800
PDGFA	NM_002607.2	TTGTTGGTGTGCCCTGGTGCCGTGGTGGCGGTCACTCCCTCTGCTGCCAGTGTTTGGACAGAACCCA	SEQ ID NO: 2801
PDGFB	NM_002608.1	ACTGAAGGAGACCCTTGGAGCCTAGGGGCATCGGCAGGAGAGTGTGTGGGCAGGGTTATTTA	SEQ ID NO: 2802
PDGFC	NM_016205.1	AGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGAC	SEQ ID NO: 2803
PDGFD	NM_025208.2	TATCGAGGCAGGTCATACCATGACCGGAAGTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGCGTTA	SEQ ID NO: 2804
PDGFRa	NM_006206.2	GGGAGTTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGAGCGTTTGGGAAGGTGGTTGAAG	SEQ ID NO: 2805
PDGFRb	NM_002609.2	CCAGCTCTCCTTCCAGCTACAGATCAATGTCCCTGTCCGAGTGCTGGAGCTAAGTGAGAGCCACCC	SEQ ID NO: 2806
PFN1	NM_005022.2	GGAAAACGTTCGTCAACATCACGCCAGCTGAGGTGGGTGTCCTGGTTGGCAAAGACCGGTCAAGTTTT	SEQ ID NO: 2807
PFN2	NM_053024.1	TCTATACGTCGATGGTGACTGCACAATGGACATCCGGACAAAGAGTCAAGGTGGGGAGCCAACATACAATGTGGCTGTCGGC	SEQ ID NO: 2808
PGK1	NM_000291.1	AGAGCCAGTTGCTGTAGAACTCAAATCTCTGCTGGGCAAGGATGTTCTGTTCTTGAAGGACTGTGTAGGCCCAG	SEQ ID NO: 2809
PI3K	NM_002646.2	TGCTACCTGGACAGCCCGTTGGTGCGCTTCCTCCTGAAACGAGCTGTGTCTGACTTGAGAGTGACTCACTACTTCTTCTGGTTACTGAAGGACGGCCT	SEQ ID NO: 2810
PI3KC2A	NM_002645.1	ATACCAATCACCGCACAAACCCAGGCTATTTGTTAAGTCCAGTCACAGCGCAAAGAAACATATGCGGAGAAAATGCTAGTGTG	SEQ ID NO: 2811
PIK3CA	NM_006218.1	GTGATTGAAGAGCATGCCAATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGAC	SEQ ID NO: 2812
PIM1	NM_002648.2	CTGCTCAAGGACACCGTCTACACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCC	SEQ ID NO: 2813
Pin1	NM_006221.1	GATCAACGGCTACATCCAGAAGATCAAGTCGGGAGAGGAGGACTTTGAGTCTCTGGCCTCACAGTTCA	SEQ ID NO: 2814
PKD1	NM_000296.2	CAGCACCAGCGATTACGACGTTGGCTGGGAGAGTCCTCACAATGGCTCGGGGACGTGGGCCTATTCAG	SEQ ID NO: 2815
PKR2	NM_002654.3	CCGCCTGGACATTGATTCACCACCCATCACAGCCCGGAACACTGGCATCATCTGTACCATTGGCCCAG	SEQ ID NO: 2816
PLA2G2A	NM_000300.2	GCATCCCTCACCCATCCTAGAGGCCAGGCAGGAGCCCTTCTATACCCACCCAGAATGAGACATCCAGCAGATTTCCAGC	SEQ ID NO: 2817
PLAUR	NM_002659.1	CCCATGGATGCTCCTCTGAAGAGACTTTCCTCATTGACTGCCGAGGCCCCATGAATCAATGTCTGGTAGCCACCGG	SEQ ID NO: 2818
PLK	NM_005030.2	AATGAATACAGTATTCCCAAGCACATCAACCCCGTGGCCGCCTCCCTCATCCAGAAGATGCTTCAGACA	SEQ ID NO: 2819
PLK3	NM_004073.2	TGAAGGAGACGTACCGCTGCATCAAGCAGGTTCACTACACGCTGCCTGCCAGCCTCTCACTGCCTG	SEQ ID NO: 2820
PLOD2	NM_000935.2	CAGGGAGGTGGTTGCAAATTTCTAAGGTACAATTGCTCTATTGAGTCACCACGAAAAGGCTGGAGCTTCATGCATCCTGGGAGA	SEQ ID NO: 2821

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
PMS1	NM_000534.2	CTTACGGTTTTCGTGGAGAAGCCTTGGGGTCAATTTGTTGTATAGCTGAGGTTTTAATTACAACAAGAACGGCTGCT	SEQ ID NO: 2822
PMS2	NM_000535.2	GATGTGGACTGCCATTCAAACCAGGAAGATACCGGATGTAAATTTCGAGTTTTGCCTCAGCCAACTAATCTCGCA	SEQ ID NO: 2823
PPARG	NM_005037.3	TGACTTTATGGAGCCCAAGTTTGAGTTTGCTGTGAAGTTCAATGCACTGGAATTAGATGACAGCGACTTGGC	SEQ ID NO: 2824
PPID	NM_005038.1	TCCTCATTTGGATGGGAAACATGTGGTGTTTGGCCAAGTAATTAAAGGAATAGGAGTGGCAAGGATATTGG	SEQ ID NO: 2825
PPM1D	NM_003620.1	GCCATCCGCAAAGGCTTTCTCGCTTGTCACCTTGCCATGTGGAAGAAACTGGCGGAATGGCC	SEQ ID NO: 2826
PPP2R4	NM_178001.1	GGCTCAGAGCATAAGGCTTCAGGGCCCAAGTTGGGAGAAGTGACCAAAGTGTAGCCAGTTTTCTGAGTTCCCGT	SEQ ID NO: 2827
PR	NM_000926.2	GCATCAGGCTGTCATTATGGTGTCCTTACCTGTGGGAGCTGTAAGGTCTTCTTTAAGAGGGCAATGGAAGGGCAGCACAACTACT	SEQ ID NO: 2828
PRDX2	NM_005809.4	GGTGTCCTTCGCCAGATCACTGTTAATGATTTGCCTGTGGGACGCTCCGTGGATGAGGCTCTGCGGCTG	SEQ ID NO: 2829
PRDX3	NM_006793.2	TGACCCCAATGGAGTCATCAAGCATTTGAGCGTCAACGATCTCCCAGTGGGCCGAAGCGTGGAAGAAACCCTCCGCTTGG	SEQ ID NO: 2830
PRDX4	NM_006406.1	TTACCCATTTGGCCTGGATTAATACCCCTCGAAGACAAGGAGGACTTGGGCCAATAAGGATTCCACTTCTTTCAG	SEQ ID NO: 2831
PRDX6	NM_004905.2	CTGTGAGCCAGAGGATGTCAGCTGCCAATTGTGTTTTCCTGCAGCAATTCCATAAACACATCCTGGTGTCATCACA	SEQ ID NO: 2832
PRKCA	NM_002737.1	CAAGCAATGCGTCATCAATGTCCCCAGCCTCTGCGGAATGGATCACACTGAGAAGAGGGGGCGGATTTAC	SEQ ID NO: 2833
PRKCB1	NM_002738.5	GACCCAGCTCCACTCCTGCTTCCAGACCATGGACCGCCTGTACTTTGTGATGGAGTACGTGAATGGG	SEQ ID NO: 2834
PRKCD	NM_006254.1	CTGACACTTGCCGCAGAGAATCCCTTTCTCACCCACCTCATCTGCACCTTCCAGACCAAGGACCACCT	SEQ ID NO: 2835
PRKR	NM_002759.1	GCGATACATGAGCCCAGAACAGATTTCTTCGCAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGGCTAATTCTTGCTGA	SEQ ID NO: 2836
pS2	NM_003225.1	GCCCTCCCAGTGTGCAAATAAGGGCTGCTGTTTCGACGACACCGTTCGTGGGGTCCCCTGGTGCTTCTATCCTAATACCATCGACG	SEQ ID NO: 2837
PTCH	NM_000264.2	CCACGACAAAGCCGACTACATGCCTGAAACAAGGCTGAGAATCCCGGCAGCAGAGCCCATCGAGTA	SEQ ID NO: 2838
PTEN	NM_000314.1	TGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCACTGTAAAGCTGGAAAGGGACGAACTGGTGTAATGATATGTGCA	SEQ ID NO: 2839
PTGER3	NM_000957.2	TAACTGGGGCAACCTTTTCTTCGCCTCTGCCTTTGCCTTCCTGGGGCTCTTGGCGCTGACAGTCACCTTTTCCTGCAA	SEQ ID NO: 2840
PTHLH	NM_002820.1	AGTGACTGGGAGTGGGCTAGAAGGGGACCACCTGTCTGACACCTCCACAACGTCGCTGGAGCTCGATTCACGGTAACAGGCTT	SEQ ID NO: 2841
PTHR1	NM_000316.1	CGAGGTACAAGCTGAGATCAAGAAATCTTGGAGCCGCTGGACACTGGCACTGGACTTCAAGCGAAAGGCACGC	SEQ ID NO: 2842
PTK2	NM_005607.3	GACCGGTCGAATGATAAGGTGTACGAGAATGTGACGGGCCTGGTGAAAGCTGTCATCGAGATGTCCAG	SEQ ID NO: 2843
PTK2B	NM_004103.3	CAAGCCCAGCCGACCTAAGTACAGACCCCCTCCGCAAACCAACCTCCTGGCTCCAAAGCTGCAGTTCCAGGTTC	SEQ ID NO: 2844
PTP4A3	NM_007079.2	AATATTTGTGCGGGGTATGGGGGTGGGTTTTTAAATCTCGTTTCTCTTGGACAAGCACAGGGATCTCGTT	SEQ ID NO: 2845
PTP4A3 v2	NM_032611.1	CCTGTTCTCGGCACCTTAAATTATTAGACCCCGGGGCAGTCAGGTGCTCCGGACACCCGAAGGCAATA	SEQ ID NO: 2846

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
PTPD1	NM_007039.2	CGCTTGCCTAACTCATACTTTCCCGTTGACACTTGATCCACG CAGCGTGGCACTGGGACGTAAGTGGCGCAGTCTGAATGG	SEQ ID NO: 2847
PTPN1	NM_002827.2	AATGAGGAAGTTTCGGATGGGGCTGATCCAGACAGCCGACC AGCTGCGCTTCTCCTACCTGGCTGTGATCGAAG	SEQ ID NO: 2848
PTPRF	NM_002840.2	TGTTTTAGCTGAGGGACGTGGTGCCGACGTCCCCA AACCTAGCTAGGCTAAGTCAAGATCAACATTCCAGGGTTGGTA	SEQ ID NO: 2849
PTPRJ	NM_002843.2	AACTTCCGGTACCTCGTTCGTGACTACATGAAGCAGA GTCCTCCCGAATCGCCGATTCTGGTGCATTGCAGTGCT	SEQ ID NO: 2850
PTPRO	NM_030667.1	CATGGCCTGATCATGGTGTGCCCACAGC AAATGCTGCAGAAAGTATCCTGCAGTTTGTACACATGG	SEQ ID NO: 2851
PTTG1	NM_004219.2	GGCTACTCTGATCTATGTTGATAAGGAAAATGGAG AACCAGGCACCCGTGTGGTTGCTAAGGATGGGCTGAAGC	SEQ ID NO: 2852
RAB32	NM_006834.2	CCTGCAGCTGTGGGACATCGCGGGGCAGGAGCGATTTGGC AACATGACCCGAGTATACTACAAGGAAGCTGTTGGTGCT	SEQ ID NO: 2853
RAB6C	NM_032144.1	GCGACAGCTCCTCTAGTTCCACCATGTCCGCGGGCGGAGACTT CGGGAATCCGCTGAGGAAATTCAAGCTGGTGTTCC	SEQ ID NO: 2854
RAC1	NM_006908.3	TGTTGTAAATGTCTCAGCCCCTCGTTCTTGGTCCTG TCCCTTGGAACCTTTGTACGCTTTGCTCAA	SEQ ID NO: 2855
RAD51C	NM_058216.1	GAACTTCTTGAGCAGGAGCATACCCAGGGCTTCATAATCA CCTTCTGTTCAGCACTAGATGATATTCTTGGGGGTGGA	SEQ ID NO: 2856
RAD54L	NM_003579.2	AGCTAGCCTCAGTGACACACATGACAGGTTGCACT GCCGACGTTGTGTCAACAGCCGTCAGATCCGG	SEQ ID NO: 2857
RAF1	NM_002880.1	CGTCGTATGCGAGAGTCTGTTTCCAGGATGCCTGTTAG TTCTCAGCACAGATATTCTACACCTCACGCCTTCA	SEQ ID NO: 2858
RALBP1	NM_006788.2	GGTGTCAGATATAAATGTGCAAATGCCTTCTTGCTGTCCTGTCGGT CTCAGTACGTTCACTTTATAGCTGCTGGCAATATCGAA	SEQ ID NO: 2859
RANBP2	NM_006267.3	TCCTTCAGCTTTCACACTGGGCTCAGAAATGAAGTTG CATGACTCTTCTGGAAGTCAGGTGGGAACAGGATTT	SEQ ID NO: 2860
ranBP7	NM_006391.1	AACATGATTATCCAAGCCGCTGGACTGCCATTGTGGACAAAATTGGCTTTTA TCTTCAGTCCGATAACAGTGCTTGTTGGC	SEQ ID NO: 2861
RANBP9	NM_005493.2	CAAGTCAGTTGAGACGCCAGTTGTGTGGAGGAAGTC AGGCCGCCATAGAAAGAATGATCCACTTTGGACGAGAGCTGCA	SEQ ID NO: 2862
RAP1GDS1	NM_021159.3	TGTGGATGCTGGATTGATTTCACCACTGGTGCAGC TGCTAAATAGCAAAGACCAGGAAGTGCTGCTT	SEQ ID NO: 2863
RARA	NM_000964.1	AGTCTGTGAGAAACGACCGAAACAAGAAGAAGAAGGAGGTGCC CAAGCCCGAGTGCTCTGAGAGCTACACGCTGACGCCG	SEQ ID NO: 2864
RARB	NM_016152.2	TGCCTGGACATCCTGATTCTTAGAATTTGCACCAGGTATACC CCAGAACAAGACACCATGACTTTCTCAGACGGCCTT	SEQ ID NO: 2865
RASSF1	NM_007182.3	AGTGGGAGACACCTGACCTTTCTCAAGCTGAGATTG AGCAGAAGATCAAGGAGTACAATGCCCAGATCA	SEQ ID NO: 2866
RBM5	NM_005778.1	CGAGAGGGAGAGCAAGACCATCATGCTGCGCGGCCTT CCCATCACCATCACAGAGAGCGATATTCGAGA	SEQ ID NO: 2867
RBX1	NM_014248.2	GGAACCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCA GGCGTCCGCTACTTCAGAAGAGTGTACTGTCGCATG	SEQ ID NO: 2868
RCC1	NM_001269.2	GGGCTGGGTGAGAATGTGATGGAGAGGAAGAAGCCG GCCCTGGTATCCATTCCGGAGGATGTTGTG	SEQ ID NO: 2869
REG4	NM_032044.2	TGCTAACTCCTGCACAGCCCCGTCCTCTTCCTTTCTGCTAGCCTGGC TAAATCTGCTCATTATTTCAGAGGGGAAACCTAGCA	SEQ ID NO: 2870
RFC	NM_003056.1	TCAAGACCATCATCACTTTCATTGTCTCGGA CGTGCGGGGCCTGGGCCTCCCGGTCCGCA AGCAGTTCCAGTTATACTCCGTGTACTTCCTGATCC	SEQ ID NO: 2871

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
RhoB	NM_004040.2	AAGCATGAACAGGACTTGACCATCTTTCCAACCCC TGGGGAAGACATTTGCAACTGACTTGGGGAGG	SEQ ID NO: 2872
rhoC	NM_175744.1	CCCGTTCGGTCTGAGGAAGGCCGGGACATGGCGAAC CGGATCAGTGCCTTTGGCTACCTTGAGTGCTC	SEQ ID NO: 2873
RIZ1	NM_012231.1	CCAGACGAGCGATTAGAAGCGGCAGCTTGTGAGGTGAAT GATTTGGGGGAAGAGGAGGAGGAGGAAGAGGAGGA	SEQ ID NO: 2874
RNF11	NM_014372.3	ACCCTGGAAGAGATGGATCAGAAAAAAAGATCCGGGAGTGTGTGAT CTGTATGATGGACTTTGTTTATGGGGACCCAAT	SEQ ID NO: 2875
ROCK1	NM_005406.1	TGTGCACATAGGAATGAGCTTCAGATGCAGTTGGCCAGCAAA GAGAGTGATATTGAGCAATTGCGTGCTAAAC	SEQ ID NO: 2876
ROCK2	NM_004850.3	GATCCGAGACCCTCGCTCCCCCATCAACGTGGAG AGCTTGCTGGATGGCTTAAATTCCTTGGTCCT	SEQ ID NO: 2877
RPLPO	NM_001002.2	CCATTCTATCATCAACGGGTACAAACGAGTCCTGGCCTTGTCTG TGGAGACGGATTACACCTTCCCACTTGCTGA	SEQ ID NO: 2878
RPS13	NM_001017.2	CAGTCGGCTTTACCCTATCGACGCAGCGTCCC CACTTGGTTGAAGTTGACATCTGACGACGTGAAGGAGCAGA	SEQ ID NO: 2879
RRM1	NM_001033.1	GGGCTACTGGCAGCTACATTGCTGGGACTAATGGCA ATTCCAATGGCCTTGTACCGATGCTGAGAG	SEQ ID NO: 2880
RRM2	NM_001034.1	CAGCGGGATTAAACAGTCCTTTAACCAGCACAGC CAGTTAAAAGATGCAGCCTCACTGCTTCAACGCAGAT	SEQ ID NO: 2881
RTN4	NM_007008.1	GACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGC TTTCATTGACAGTATTCAGCATTGTGAGCGTAACAG	SEQ ID NO: 2882
RUNX1	NM_001754.2	AACAGAGACATTGCCAACCATATTGGATCTGCTTGC TGTCCAAACCAGCAAACTTCCTGGGCAAATCAC	SEQ ID NO: 2883
RXRA	NM_002957.3	GCTCTGTTGTGTCCTGTTGCCGGCTCTGGCCTTC CTGTGACTGACTGTGAAGTGGCTTCTCCGTAC	SEQ ID NO: 2884
S100A1	NM_006271.1	TGGACAAGGTGATGAAGGAGCTAGACGAGAATGGAGAC GGGGAGGTGGACTTCCAGGAGTATGTGGTGCT	SEQ ID NO: 2885
S100A2	NM_005978.2	TGGCTGTGCTGGTCACTACCTTCCACAAGTACTCCTGCCAAGA GGGCGACAAGTTCAAGCTGAGTAAGGGGGA	SEQ ID NO: 2886
S100A4	NM_002961.2	GACTGCTGTCATGGCGTGCCCTCTGGAGAAGGCC CTGGATGTGATGGTGTCCACCTTCCACAAGTACTCG	SEQ ID NO: 2887
S100A8	NM_002964.3	ACTCCCTGATAAAGGGGAATTTCCATGCCGTCTA CAGGGATGACCTGAAGAAATTGCTAGAGACCGAGTGTCCTCA	SEQ ID NO: 2888
S100A9	NM_002965.2	CTTTGGGACAGAGTGCAAGACGATGACTTGC AAAATGTCGCAGCTGGAACGCAACATAGAGACCA	SEQ ID NO: 2889
S100P	NM_005980.2	AGACAAGGATGCCGTGGATAAATTGCTCAAGGACCT GGACGCCAATGGAGATGCCCAGGTGGACTTC	SEQ ID NO: 2890
SAT	NM_002970.1	CCTTTTACCACTGCCTGGTTGCAGAAGTGCCGAAAG AGCACTGGACTCCGGAAGGACACAGCATTGT	SEQ ID NO: 2891
SBA2	NM_018639.3	GGACTCAACGATGGGCAGATCAAGATCTGGGA GGTGCAGACAGGGCTCCTGCTTTTGAATCTTTCCG	SEQ ID NO: 2892
SDC1	NM_002997.1	GAAATTGACGAGGGGTGTCTTGGGCAGAGCTGGCTCTGAGCGCCT CCATCCAAGGCCAGGTTCTCCGTTAGCTCCT	SEQ ID NO: 2893
SEMA3B	NM_004636.1	GCTCCAGGATGTGTTTCTGTTGTCCTCGCGGGAC CACCGGACCCCGCTGCTCTATGCCGTCTTCTCCACGT	SEQ ID NO: 2894
SEMA3F	NM_004186.1	CGCGAGCCCCTCATTATACACTGGGCAGCCTCCCCACAG CGCATCGAGGAATGCGTGCTCTCAGGCAAGGATGTCAACGGCGAGTG	SEQ ID NO: 2895
SEMA4B	NM_020210.1	TTCCAGCCCAACACAGTGAACACT TTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGACTC	SEQ ID NO: 2896

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
SFRP2	NM_003013.2	CAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAAATCGGTGCTGTGGCTCAAAGACAGCTTGCA	SEQ ID NO: 2897
SFRP4	NM_003014.2	TACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCATGTGCCCCTTGCCCTAACAAC	SEQ ID NO: 2898
SGCB	NM_000232.1	CAGTGGAGACCAGTTGGGTAGTGGTGACTGGGTACGCTACAAGCTCTGCATGTGTGCTGATGGGACGCTCTTCAAGG	SEQ ID NO: 2899
SHC1	NM_003029.3	CCAACACCTTCTTGGCTTCTGGGACCTGTGTTCTTGCTGAGCACCCTCTCCGGTTTGGGTTGGGATAACAG	SEQ ID NO: 2900
SHH	NM_000193.2	GTCCAAGGCACATATCCACTGCTCGGTGAAAGCAGAGAACTCGGTGGCGGCCAAATCGGGAGGCTGCTTC	SEQ ID NO: 2901
SI	NM_001041.1	AACGGACTCCCTCAATTTGTGCAAGATTTGCATGACCATGGACAGAAATATGTCATCATCTTGGACCCTGCAATTTC	SEQ ID NO: 2902
Siah-1	NM_003031.2	TTGGCATTGGAACTACATTCAATCCGCGGTATCCTCGGATTAGTTCTAGGACCCCCTTCTCCATACC	SEQ ID NO: 2903
SIAT4A	NM_003033.2	AACCACAGTTGGAGGAGGACGGCAGAGACAGTTTCCCTCCCCGCTATACCAACACCCTTCCTTCG	SEQ ID NO: 2904
SIAT7B	NM_006456.1	TCCAGCCCAAATCCTCCTGGTGGCACATCCTACCCCAGATGCTAAAGTGATTCAAGGACTCCAGGACACC	SEQ ID NO: 2905
SIM2	NM_005069.2	GATGGTAGGAAGGGATGTGCCCGCCTCTCCACGCACTCAGCTATACCTCATTCACAGCTCCTTGTG	SEQ ID NO: 2906
SIN3A	NM_015477.1	CCAGAGTCATGCTCATCCAGCCCCACCAGTTGCACCAGTGCAGGGACAGCAGCAATTTCAGAGGCTGAAGGTGG	SEQ ID NO: 2907
SIR2	NM_012238.3	AGCTGGGGTGTCTGTTTCATGTGGAATACCTGACTTCAGGTCAAGGGATGGTATTTATGCTCGCCTTGCTGT	SEQ ID NO: 2908
SKP1A	NM_006930.2	CCATTGCCTTTGCTTTGTTCATAATTTCAGCAGGGCAGAATAAAAACCATGGGAGGCAAAGAAAGGAAATCCGGAA	SEQ ID NO: 2909
SKP2	NM_005983.2	AGTTGCAGAATCTAAGCCTGGAAGGCCTGCGGCTTTCGGATCCCATTGTCAATACTCTCGCAAAAAACTCA	SEQ ID NO: 2910
SLC25A3	NM_213611.1	TCTGCCAGTGCTGAATTCTTTGCTGACATTGCCCTGGCTCCTATGGAAGCTGCTAAGGTTCGAA	SEQ ID NO: 2911
SLC2A1	NM_006516.1	GCCTGAGTCTCCTGTGCCCACATCCCAGGCTTCACCCTGAATGGTTCCATGCCTGAGGGTGGAGACT	SEQ ID NO: 2912
SLC31A1	NM_001859.2	CCGTTCGAAGAGTCGTGAGGGGGTGACGGGTTAAGATTCGGAGAGAGAGGTGCTAGTGGCTGGACT	SEQ ID NO: 2913
SLC5A8	NM_145913.2	CCTGCTTTCAACCACATTGAATTGAACTCAGATCAGAGTGGCAAGAGCAATGGGACTCGTTTGTGAAGCTGCTCT	SEQ ID NO: 2914
SLC7A5	NM_003486.4	GCGCAGAGGCCAGTTAAAGTAGATCACCTCCTCGAACCCACTCCGGTTCCCCGCAACCCACAGCTCAGCT	SEQ ID NO: 2915
SLPI	NM_003064.2	ATGGCCAATGTTTGATGCTTAACCCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAAGCGTGACTTGAAGTGT	SEQ ID NO: 2916
SMARCA3	NM_003071.2	AGGGACTGTCCTGGCACATTATGCAGATGTCCTGGGTCTTTTGCTTAGACTGCGGCAAATTTGTTG	SEQ ID NO: 2917
SNAI1	NM_005985.2	CCCAATCGGAAGCCTAACTACAGCGAGCTGCAGGACTCTAATCCAGAGTTTACCTTCCAGCAGCCCTAC	SEQ ID NO: 2918
SNAI2	NM_003068.3	GGCTGGCCAAACATAAGCAGCTGCACTGCGATGCCCAGTCTAGAAAATCTTTCAGCTGTAAATACTGTGACAAGGA	SEQ ID NO: 2919
SNRPF	NM_003095.1	GGCTGGTCGGCAGAGAGTAGCCTGCAACATTCGGCCGTGGTTTACATGAGTTTACCCCTCAATCCCAAACCTTTCCTCA	SEQ ID NO: 2920
SOD1	NM_000454.3	TGAAGAGAGGCATGTTGGAGACTTGGGCAATGTGACTGCTGACAAAGATGGTGTGGCCGATGTGTCTATT	SEQ ID NO: 2921

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
SOD2	NM_000636.1	GCTTGTCCAAATCAGGATCCACTGCAAGGAACAACAGGCCTTATTCCACTGCTGGGGATTGATGTGTGGGAGCACGCT	SEQ ID NO: 2922
SOS1	NM_005633.2	TCTGCACCAAATTCTCCAAGAACACCGTTAACACCTCCGCCTGCTTCTGGTGCTTCCAGTACCAC	SEQ ID NO: 2923
SOX17	NM_022454.2	TCGTGTGCAAGCCTGAGATGGGCCTCCCCTACCAGGGGCATGACTCCGGTGTGAATCTCCCCGACAG	SEQ ID NO: 2924
SPARC	NM_003118.1	TCTTCCCTGTACACTGGCAGTTCGGCCAGCTGGACCAGCACCCCATTGACGGGTACCTCTCCCACACCGAGCT	SEQ ID NO: 2925
SPIND2	NM_021102.1	AGGAATGCAGCGGATTCCTCTGTCCCAAGTGCTCCCAGAAGGCAGGATTCTGAAGACCACTCCAGCGA	SEQ ID NO: 2926
SPRY1	AK026960.1	CAGACCAGTCCCTGGTCATAGGTCTGAAAGGGCAATCCGGACCCAGCCCAAGCAACTGATTGTGGATGACTTGAAGG	SEQ ID NO: 2927
SPRY2	NM_005842.1	TGTGGCAAGTGCAAATGTAAGGAGTGCACCTACCCAAGGCCTCTGCCATCAGACTGGATCTGCGAC	SEQ ID NO: 2928
SR-A1	NM_021228.1	AGATGGAAGAAGCCAACCTGGCGAGCCGAGCGAAGGCCCAGGAGCTGATCCAGGCCACCAACCAGATCCTCAGCCACAG	SEQ ID NO: 2929
ST14	NM_021978.2	TGACTGCACATGGAACATTGAGGTGCCCAACAACCAGCATGTGAAGGTGCGCTTCAAATTCTT	SEQ ID NO: 2930
STAT1	NM_007315.1	GGGCTCAGCTTTCAGAAGTGCTGAGTTGGCAGTTTTCTTCTGTCACCAAAAGAGGTCTCAATGTGGACCAGCTGAACATGT	SEQ ID NO: 2931
STAT3	NM_003150.1	TCACATGCCACTTTGGTGTTTCATAATCTCCTGGGAGAGATTGACCAGCAGTATAGCCGCTTCCTGCAAG	SEQ ID NO: 2932
STAT5A	NM_003152.1	GAGGCGCTCAACATGAAATTCAAGGCCGAAGTGCAGAGCAACCGGGGCCTGACCAAGGAGAACCTCGTGTTCCTGGC	SEQ ID NO: 2933
STAT5B	NM_012448.1	CCAGTGGTGGTGATCGTTCATGGCAGCCAGGACAACAATGCGACGGCCACTGTTCTCTGGGACAATGCTTTTGC	SEQ ID NO: 2934
STC1	NM_003155.1	CTCCGAGGTGAGGAGGACTCTCCCTCCCACATCAAACGCACATCCCATGAGAGTGCATAACCAGGGAGAGGT	SEQ ID NO: 2935
STK11	NM_000455.3	GGACTCGGAGACGCTGTGCAGGAGGGCCGTCAAGATCCTCAAGAAGAAGAAGTTGCGAAGGATCCC	SEQ ID NO: 2936
STK15	NM_003600.1	CATCTTCCAGGAGGACCACTCTCTGTGGCACCCTGGACTACCTGCCCCCTGAAATGATTGAAGGTCGGA	SEQ ID NO: 2937
STMN1	NM_005563.2	AATACCCAACGCACAAATGACCGCACGTTCTCTGCCCCGTTTCTTGCCCCAGTGTGGTTTGCATTGTCTCC	SEQ ID NO: 2938
STMY3	NM_005940.2	CCTGGAGGCTGCAACATACCTCAATCCTGTCCCAGGCCGGATCCTCCTGAAGCCCTTTTCGCAGCACTGCTATCCTCCAAAGCCATTGTA	SEQ ID NO: 2939
STS	NM_000351.2	GAAGATCCCTTTCCTCCTACTGTTCTTTCTGTGGGAAGCCGAGAGCCACGAAGCATCAAGGCCGAACATCATCC	SEQ ID NO: 2940
SURV	NM_001168.1	TGTTTTGATTCCCGGGCTTACCAGGTGAGAAGTGAGGGAGGAAGAAGGCAGTGTCCCTTTTGCTAGAGCTGACAGCTTTG	SEQ ID NO: 2941
TAGLN	NM_003186.2	GATGGAGCAGGTGGCTCAGTTCCTGAAGGCGGCTGAGGACTCTGGGGTCATCAAGACTGACATGTTCCAGACT	SEQ ID NO: 2942
TBP	NM_003194.1	GCCCGAAACGCCGAATATAATCCCAAGCGGTTTGCTGCGGTAATCATGAGGATAAGAGAGCCACG	SEQ ID NO: 2943
TCF-1	NM_000545.3	GAGGTCCTGAGCACTGCCAGGAGGGACAAAGGAGCCTGTGAACCCAGGACAAGCATGGTCCCACATC	SEQ ID NO: 2944
TCF-7	NM_003202.2	GCAGCTGCAGTCAACAGTTCAAAGAAGTCATGGCCCAAATCCAGTGTGCACCCCTCCCCATTCACAG	SEQ ID NO: 2945
TCF7L1	NM_031283.1	CCGGGACACTTTCCAGAAGCCGCGGGACTATTTCGCCGAAGTGAGAAGGCCTCAGGACAGCGCGTTCT	SEQ ID NO: 2946

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
TCF7L2	NM_030756.1	CCAATCACGACAGGAGGATTCAGACACCCCTACCCCACAGCTCTGACCGTCAATGCTTCCGTGTCCA	SEQ ID NO: 2947
TCFL4	NM_170607.2	CTGACTGCTCTGCTTAAAGGTGAAAGTAGCAGGAACAACAACAAAAGCCAACCAAAAACAAGGTAGCCAGTGCAAGACAT	SEQ ID NO: 2948
TEK	NM_000459.1	ACTTCGGTGCTACTTAACAACTTACATCCCAGGGAGCAGTACGTGGTCCGAGCTAGAGTCAACACCAAGGCCCAGG	SEQ ID NO: 2949
TERC	U86046.1	AAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACAT	SEQ ID NO: 2950
TERT	NM_003219.1	GACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTC	SEQ ID NO: 2951
TFF3	NM_003226.1	AGGCACTGTTCATCTCAGTTTTTCTGTCCCTTTGCTCCCGGCAAGCTTTCTGCTGAAAGTTCATATCTGGAGCCTGATG	SEQ ID NO: 2952
TGFA	NM_003236.1	GGTGTGCCACAGACCTTCCTACTTGGCCTGTAATCACCTGTGCAGCCTTTTGTGGGCCTTCAAAACTCTGTCAAGAACTCCGT	SEQ ID NO: 2953
TGFB2	NM_003238.1	ACCAGTCCCCCAGAAGACTATCCTGAGCCCGAGGAAGTCCCCCCGGAGGTGATTTCCATCTACAACAGCACCAGG	SEQ ID NO: 2954
TGFB3	NM_003239.1	GGATCGAGCTCTTCCAGATCCTTCGGCCAGATGAGCACATTGCCAAACAGCGCTATATCGGTGGC	SEQ ID NO: 2955
TGFBI	NM_000358.1	GCTACGAGTGCTGTCCTGGATATGAAAAGGTCCCTGGGGAGAAGGGCTGTCCAGCAGCCCTACCACT	SEQ ID NO: 2956
TGFBR1	NM_004612.1	GTCATCACCTGGCCTTGGTCCTGTGGAACTGGCAGCTGTCATTGCTGGACCAGTGTGCTTCGTCTGC	SEQ ID NO: 2957
TGFBR2	NM_003242.2	AACACCAATGGGTTCCATCTTTCTGGGCTCCTGATTGCTCAAGCACAGTTTGGCCTGATGAAGAGG	SEQ ID NO: 2958
THBS1	NM_003246.1	CATCCGCAAAGTGACTGAAGAGAACAAAGAGTTGGCCAATGAGCTGAGGCGGCCTCCCCTATGCTATCACAACGGAGTTCAGTAC	SEQ ID NO: 2959
THY1	NM_006288.2	GGACAAGACCCTCTCAGGCTGTCCCAAGCTCCCAAGAGCTTCCAGAGCTCTGACCCACAGCCTCCAA	SEQ ID NO: 2960
TIMP1	NM_003254.1	TCCCTGCGGTCCCAGATAGCCTGAATCCTGCCCGGAGTGGAACTGAAGCCTGCACAGTGTCCACCCTGTTCCCAC	SEQ ID NO: 2961
TIMP2	NM_003255.2	TCACCCTCTGTGACTTCATCGTGCCCTGGGACACCCTGAGCACCACCCAGAAGAAGAGCCTGAACCACA	SEQ ID NO: 2962
TIMP3	NM_000362.2	CTACCTGCCTTGCTTTGTGACTTCCAAGAACGAGTGTCTCTGGACCGACATGCTCTCCAATTTCGGT	SEQ ID NO: 2963
TJP1	NM_003257.1	ACTTTGCTGGGACAAAGGTCAACTGAAGAAGTGGGCAGGCCCGAGGCAGGAGAGATGCTGAGGAGTCCATGTG	SEQ ID NO: 2964
TK1	NM_003258.1	GCCGGGAAGACCGTAATTGTGGCTGCACTGGATGGGACCTTCCAGAGGAAGCCATTTGGGGCCATCCTGAACCTGGTGCCGCTG	SEQ ID NO: 2965
TLN1	NM_006289.2	AAGCAGAAGGGAGAGCGTAAGATCTTCCAGGCACACAAGAATTGTGGGCAGATGAGTGAGATTGAGGCCAAGG	SEQ ID NO: 2966
TMEPAI	NM_020182.3	CAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGTCAGGCAACGGAATCCCAGAGCCGCAGGTCTAC	SEQ ID NO: 2967
TMSB10	NM_021103.2	GAAATCGCCAGCTTCGATAAGGCCAAGCTGAAGAAAACGGAGACGCAGGAAAAGAACACCCTGCCGAC	SEQ ID NO: 2968
TMSB4X	NM_021109.2	CACATCAAAGAACTACTGACAACGAAGGCCGCGCCTGCCTTTCCCATCTGTCTATCTATCTGGCTGGCAGG	SEQ ID NO: 2969
TNC	NM_002160.1	AGCTCGGAACCTCACCGTGCCTGGCAGCCTTCGGGCTGTGGACATACCGGGCCTCAAGGCTGCTAC	SEQ ID NO: 2970
TNF	NM_000594.1	GGAGAAGGGTGACCGACTCAGCGCTGAGATCAATCGGCCCGACTATCTCGACTTTGCCGAGTCTGGGCA	SEQ ID NO: 2971

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
TNFRSF5	NM_001250.3	TCTCACCTCGCTATGGTTCGTCTGCCTCTGCAGTGCGTCC TCTGGGGCTGCTTGCTGACCGCTGTCCATC	SEQ ID NO: 2972
TNFRSF6B	NM_003823.2	CCTCAGCACCAGGGTACCAGGAGCTGAGGAGTG TGAGCGTGCCGTCATCGACTTTGTGGCTTTCCAGGACA	SEQ ID NO: 2973
TNFSF4	NM_003326.2	CTTCATCTTCCCTCTACCCAGATTGTGAAGATGGAAAGGGT CCAACCCCTGGAAGAGAATGTGGGAAATGCAGC	SEQ ID NO: 2974
TOP2A	NM_001067.1	AATCCAAGGGGGAGAGTGATGACTTCCATATGGACTTTGA CTCAGCTGTGGCTCCTCGGGCAAAATCTGTAC	SEQ ID NO: 2975
TOP2B	NM_001068.1	TGTGGACATCTTCCCCTCAGACTTCCCTACTGAGC CACCTTCTCTGCCACGAACCGGTCGGGCTAG	SEQ ID NO: 2976
TP	NM_001953.2	CTATATGCAGCCAGAGATGTGACAGCCACCGTGGACAGCCTGCCACTC ATCACAGCCTCCATTCTCAGTAAGAAACTCGTGG	SEQ ID NO: 2977
TP53BP1	NM_005657.1	TGCTGTTGCTGAGTCTGTTGCCAGTCCCCAGAA GACCATGTCTGTGTTGAGCTGTATCTGTGAAGCCAGGCAAG	SEQ ID NO: 2978
TP53BP2	NM_005426.1	GGGCCAAATATTCAGAAGCTTTTATATCAGAGGACCACCA TAGCGGCCATGGAGACCATCTCTGTCCCATCATACCCATCC	SEQ ID NO: 2979
TP53I3	NM_004881.2	GCGGACTTAATGCAGAGACAAGGCCAGTATGAC CCACCTCCAGGAGCCAGCAACATTTTGGGACTTGA	SEQ ID NO: 2980
TRAG3	NM_004909.1	GACGCTGGTCTGGTGAAGATGTCCAGGAAACCA CGAGCCTCCAGCCCATTGTCCAACAACCACCCA	SEQ ID NO: 2981
TRAIL	NM_003810.1	CTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTA CGTGTACTTTACCAACGAGCTGAAGCAGATG	SEQ ID NO: 2982
TS	NM_001071.1	GCCTCGGTGTGCCTTTCAACATCGCCAGCTACGCC CTGCTCACGTACATGATTGCGCACATCACG	SEQ ID NO: 2983
TST	NM_003312.4	GGAGCCGGATGCAGTAGGACTGGACTCGGGCCA TATCCGTGGTGCCGTCAACATGCCTTTCATGGACTT	SEQ ID NO: 2984
TUBA1	NM_006000.1	TGTCACCCCGACTCAACGTGAGACGCACCGCCC GGACTCACCATGCGTGAATGCATCTCAGTCCACGT	SEQ ID NO: 2985
TUBB	NM_001069.1	CGAGGACGAGGCTTAAAAACTTCTCAGATCAATCGT GCATCCTTAGTGAACTTCTGTTGTCCTCAAGCATGGT	SEQ ID NO: 2986
TUFM	NM_003321.3	GTATCACCATCAATGCGGCTCATGTGGAGTATAGCACT GCCGCCCGCCACTACGCCCACACAGACTG	SEQ ID NO: 2987
TULP3	NM_003324.2	TGTGTATAGTCCTGCCCCTCAAGGTGTCACAGT AAGATGTCGGATAATCCGGGATAAAAGGGGAATGGATCGGG	SEQ ID NO: 2988
tusc4	NM_006545.4	GGAGGAGCTAAATGCCTCAGGCCGGTGCACTCT GCCCATTGATGAGTCCAACACCATCCACTTGAAGG	SEQ ID NO: 2989
UBB	NM_018955.1	GAGTCGACCCTGCACCTGGTCCTGCGTCTGA GAGGTGGTATGCAGATCTTCGTGAAGACCCTGACCGGCA AGACCATCACCCTGGAAGTGGAGCCCAGTGACACCAT CGAAAATGTGAAGGCCAAGATCCAGGATAAAGAA GGCATCCCTCCCGACCAGCAGAGGCTCATCTTTGC AGGCAAGCAGCTGGAAGATGGCCGCACTCTTTCTG ACTACAACATCCAGAAGGAGTCGACCCTGCACCTGG TCCTGCGTCTGAGAGGTGGTATGCAGATCTTCGTG AAGACCCTGACCGGCAAGACCATCACTCTGGAAGTG GAGCCCAGTGACACCATCGAAAATGTGAAGGCCA AGATCCAAGATAAAGAAGGCATCCCTCCCGACCAG CAGAGGCTCATCTTTGCAGGCAAGCAGCTGGAAGAT GGCCGCACTCTTTCTGACTACAACATCCAGAAGGAGT CGACCCTGCACCTGGTCCTGCGCCTGAGGGGTG GCTGTTAATTCTTCAGTCATGGCATTCGC	SEQ ID NO: 2990
UBC	NM_021009.2	ACGCACCCTGTCTGACTACAACATCCAGAAAGA GTCCACCCTGCACCTGGTGCTCCGTCTTAGAGGT	SEQ ID NO: 2991
UBE2C	NM_007019.2	TGTCTGGCGATAAAGGGATTTCTGCCTTCCC TGAATCAGACAACCTTTTCAAATGGGTAGGGACCAT	SEQ ID NO: 2992

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
UBE2M	NM_003969.1	CTCCATAATTTATGGCCTGCAGTATCTCTTCTTGGAGCCCAACCCCGAGGACCCACTGAACAAGGAGGCCGCA	SEQ ID NO: 2993
UBL1	NM_003352.3	GTGAAGCCACCGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACTTGGGGGATAAGAAGGAAGG	SEQ ID NO: 2994
UCP2	NM_003355.2	ACCATGCTCCAGAAGGAGGGGCCCCGAGCCTTCTACAAAGGGTTCATGCCCTCCTTTCTCCGCTTGGGTT	SEQ ID NO: 2995
UGT1A1	NM_000463.2	CCATGCAGCCTGGAATTTGAGGCTACCCAGTGCCCCAACCCATTCTCCTACGTGCCCAGGCCTCTC	SEQ ID NO: 2996
UMPS	NM_000373.1	TGCGGAAATGAGCTCCACCGGCTCCCTGGCCACTGGGGACTACACTAGAGCAGCGGTTAGAATGGCTGAGG	SEQ ID NO: 2997
UNC5A	XM_030300.7	GACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCAT	SEQ ID NO: 2998
UNC5B	NM_170744.2	AGAACGGAGGCCGTGACTGCAGCGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTGTGCATG	SEQ ID NO: 2999
UNC5C	NM_003728.2	CTGAACACAGTGGAGCTGGTTTGCAAACTCTGTGTGCGGCAGGTGGAAGGAGAAGGGCAGATCTTCCAG	SEQ ID NO: 3000
upa	NM_002658.1	GTGGATGTGCCCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTACCCTGGATCCGCAG	SEQ ID NO: 3001
UPP1	NM_003364.2	ACGGGTCCTGCCTCAGTTGGCGGAATGGCGGCCACGGGAGCCAATGCAGAGAAAGCTGAAAGTCACAATGATTGCCCCG	SEQ ID NO: 3002
VCAM1	NM_001078.2	TGGCTTCAGGAGCTGAATACCCTCCCAGGCACACACAGGTGGGACACAAATAAGGGTTTTGGAACCACTATTTTCTCATCACGACAGCA	SEQ ID NO: 3003
VCL	NM_003373.2	GATACCACAACTCCCATCAAGCTGTTGGCAGTGGCAGCCACGGCGCCTCCTGATGCGCCTAACAGGGA	SEQ ID NO: 3004
VCP	NM_007126.2	GGCTTTGGCAGCTTCAGATTCCCTTCAGGGAACCAGGGTGGAGCTGGCCCCAGTCAGGGCAGTGGAG	SEQ ID NO: 3005
VDAC1	NM_003374.1	GCTGCGACATGGATTTCGACATTGCTGGGCCTTCCATCCGGGGTGCTCTGGTGCTAGGTTACGAGGGCTGG	SEQ ID NO: 3006
VDAC2	NM_003375.2	ACCCACGGACAGACTTGCGCGCGTCCAATGTGTATTCCTCCATCATATGCTGACCTTGGCAAAGCT	SEQ ID NO: 3007
VDR	NM_000376.1	GCCCTGGATTTCAGAAAGAGCCAAGTCTGGATCTGGGACCCTTTCCTTCCTTCCCTGGCTTGTAACT	SEQ ID NO: 3008
VEGF	NM_003376.3	CTGCTGTCTTGGGTGCATTGGAGCCTTGCCTTGCTGCTCTACCTCCACCATGCCAAGTGGTCCCAGGCTGC	SEQ ID NO: 3009
VEGF_altsplice1	AF486837.1	TGTGAATGCAGACCAAAGAAAGATAGAGCAAGACAAGAAAATCCCTGTGGGCCTTGCTCAGAGCGGAGAAAGC	SEQ ID NO: 3010
VEGF_altsplice2	AF214570.1	AGCTTCCTACAGCACAACAAATGTGAATGCAGACCAAAGAAAGATAGAGCAAGACAAGAAAAATGTGACAAGCCGAG	SEQ ID NO: 3011
VEGFB	NM_003377.2	TGACGATGGCCTGGAGTGTGTGCCCACTGGGCAGCACCAAGTCCGGATGCAGATCCTCATGATCCGGTACC	SEQ ID NO: 3012
VEGFC	NM_005429.2	CCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCACACTT	SEQ ID NO: 3013
VIM	NM_003380.1	TGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGC	SEQ ID NO: 3014
WIF	NM_007191.2	TACAAGCTGAGTGCCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG	SEQ ID NO: 3015
WISP1	NM_003882.2	AGAGGCATCCATGAACTTCACACTTGCGGGCTGCATCAGCACACGCTCCTATCAACCCAAGTACTGTGGAGTTTG	SEQ ID NO: 3016
Wnt-3a	NM_033131.2	ACAAAGCTACCAGGGAGTCGGCCTTTGTCCACGCCATTGCCTCAGCCGGTGTGGCCTTTGCAGTGACACGCTCA	SEQ ID NO: 3017

TABLE B-continued

Gene	Locus Link	Sequence	Sequence ID Number
Wnt-5a	NM_003392.2	GTATCAGGACCACATGCAGTACATCGGAGAAGGCGCGAAGACAGGCATCAAAGAATGCCAGTATCAATTCCGACA	SEQ ID NO: 3018
Wnt-5b	NM_032642.2	TGTCTTCAGGGTCTTGTCCAGAATGTAGATGGGTTCCGTAAGAGGCCTGGTGCTCTCTTACTCTTTCATCCACGTGCAC	SEQ ID NO: 3019
WND2	NM_003391.1	CGGTGGAATCTGGCTCTGGCTCCCTCTGCTCTTGACCTGGCTCACCCCCGAGGTCAACTCTTCATGG	SEQ ID NO: 3020
WWOX	NM_016373.1	ATCGCAGCTGGTGGGTGTACACACTGCTGTTTACCTTGGCGAGGCCTTTCACCAAGTCCATGCAACAGGGAGCT	SEQ ID NO: 3021
XPA	NM_000380.2	GGGTAGAGGGAAAAGGGTTCAACAAAGGCTGAACTGGATTCTTAACCAAGAAACAAATAATAGCAATGGTGGTGCA	SEQ ID NO: 3022
XPC	NM_004628.2	GATACATCGTCTGCGAGGAATTCAAAGACGTGCTCCTGACTGCCTGGGAAAATGAGCAGGCAGTCATTGAAAG	SEQ ID NO: 3023
XRCC1	NM_006297.1	GGAGATGAAGCCCCCAAGCTTCCTCAGAAGCAACGCCAGACCAAAACCAAGCCCACTCAGGCAGCTGGAC	SEQ ID NO: 3024
YB-1	NM_004559.1	AGACTGTGGAGTTTGATGTTGTTGAAGGAGAAAAGGGTGCGGAGGCAGCAAATGTTACAGGTCCTGGTGGTGTTCC	SEQ ID NO: 3025
YWHAH	NM_003405.2	CATGGCCTCCGCTATGAAGGCGGTGACAGAGCTGAATGAACCTCTCTCCAATGAAGATCGAAATCTCC	SEQ ID NO: 3026
zbtb7	NM_015898.2	CTGCGTTCACACCCCAGTGTCACAGGGCGAGCTGTTCTGGAGAGAAAACCATCTGTCGTGGCTGAG	SEQ ID NO: 3027
ZG16	NM_152338.1	TGCTGAGCCTCCTCTCCTTGGCAGGGGCACTGTGATGAGGAGTAAGAACTCCCTTATCACTAACCCCCATCC	SEQ ID NO: 3028

SEQUENCE LISTING

The patent contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US07695913B2). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed:

1. A method of predicting clinical outcome for a human subject diagnosed with colorectal cancer following surgical resection of said cancer, comprising:

assaying a normalized expression level of an RNA transcript, or an expression product thereof, of INHBA, MYBL2, FAP and Ki67 in a biological sample comprising colorectal cancer cells obtained from the human subject;

determining a likelihood of a positive clinical outcome for the human subject based on the normalized expression, wherein

(a) normalized expression of each of INHBA and FAP is negatively correlated with an increased likelihood of a positive clinical outcome; and

(b) normalized expression of each of MYBL2 and Ki67 is positively correlated with an increased likelihood of a positive clinical outcome; and

providing a report comprising a score, wherein the score is indicative of the likelihood of a positive clinical outcome in the human subject.

2. The method of claim **1** wherein evidence of said normalized expression level is obtained by a method of gene expression profiling.

3. The method of claim **2** wherein said method is a PCR-based method.

4. The method of claim **3** wherein said normalized expression level is normalized relative to the expression level of one or more reference genes, or their expression products.

5. The method of claim **1** wherein said positive clinical outcome is expressed in terms of Recurrence-Free Interval (RFI), Disease-Free Survival (DFS), or Distant Recurrence-Free Interval (DRFI).

6. The method of claim **1** wherein said cancer is Dukes B (stage II) or Dukes C (stage III) colorectal cancer.

7. The method of claim **6** wherein said cancer is Dukes B (stage II) or Dukes C (stage III) colon cancer.

8. The method of claim **1**, wherein said assaying comprises assaying a normalized expression level of an RNA transcript, or an expression product thereof, of one or more of BGN, GADD45B, COL1A1, SPARC, COL1A2, and CYMC in the biological sample, wherein

(a) normalized expression of each of BGN, GADD45B, COL1A1, SPARC, and COL1A2 is negatively correlated with an increased likelihood of a positive clinical outcome; and

(b) normalized expression of CMYC is positively correlated with an increased likelihood of a positive clinical outcome.

9. A method of predicting in a human subject diagnosed with Dukes B (stage II) or Dukes C (stage III) colorectal cancer a likelihood of recurrence of colorectal cancer following surgical resection of said cancer, comprising:

assaying a normalized expression level of an RNA transcript, or an expression product thereof, of INHBA, MYBL2, FAP and Ki67 in a biological sample comprising colorectal cancer cells obtained from the human subject, wherein

(a) normalized expression of each of INHBA and FAP is negatively correlated with a decreased likelihood of recurrence of colorectal cancer; and

(b) normalized expression of each of MYBL2 and Ki67 is positively correlated with a decreased likelihood of recurrence of colorectal cancer; and

providing a report comprising a score, wherein the score is indicative of the likelihood of a recurrence of colorectal cancer in the human subject.

10. The method of claim **9**, wherein said assaying comprises assaying a normalized expression level of an RNA transcript, or an expression product thereof, of one or more of BGN, GADD45B, COL1A1, SPARC, COL1A2, and CYMC in the biological sample, wherein

(a) normalized expression of each of BGN, GADD45B, COL1A1, SPARC, and COL1A2 is negatively correlated with a decreased likelihood of recurrence of colorectal cancer; and

(b) normalized expression of CYMC is positively correlated with a decreased likelihood of recurrence of colorectal cancer.

11. The method of claim **9** wherein evidence of said expression level is obtained by a method of gene expression profiling.

12. The method of claim **11** wherein said method is a PCR-based method.

13. The method of claim **9**, wherein, if said likelihood of recurrence is predicted to be increased, said human subject is subjected to further therapy following said surgical removal.

14. The method of claim **13** wherein said further therapy is chemotherapy and/or radiation therapy.

15. The method of claim **9**, wherein said normalized expression level is normalized relative to the expression level of one or more reference genes, or their expression products.

16. The method of claim **9** wherein, said positive clinical outcome is expressed in terms of Recurrence-Free Interval (RFI), Disease-Free Survival (DFS), or Distant Recurrence-Free Interval (DRFI).

17. The method of claim **9** wherein, said colorectal cancer is Dukes B (stage II) or Dukes C (stage III) colorectal cancer.

18. The method of claim **17** wherein said colorectal cancer is Dukes B (stage II) or Dukes C (stage III) colon cancer.

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